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(54) Title: 29 HUMAN SECRETED PROTEINS			
(57) Abstract			
<p>The present invention relates to novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.</p>			

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29 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and their production.

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or 10 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum (ER). The ER separates the membrane-bounded proteins from all other types of 15 proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

20 Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or 25 secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes 30 encoding human secreted proteins have been identified. These secreted proteins include the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying 35 and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, 5 and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

10

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original 15 environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

20 In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce 25 a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid 30 sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated 35 amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

- analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard,
- 5 Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained 10 in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the 15 filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages 20 of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even 25 lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include 30 Denhardt's reagent, BLOTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such 35 as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and 10 double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability 15 or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

20 The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, 25 as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be 30 branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a 35 nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins
5 such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990);
10 Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y"
refers to a polypeptide sequence, both sequences identified by an integer specified in
Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting
15 activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present
20 invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

25 **Polynucleotides and Polypeptides of the Invention**

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

The gene encoding the disclosed cDNA is believed to reside on chromosome 8.
30 Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 8.

This gene is expressed primarily in anergic T cell, and to a lesser extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune or hematopoietic disorders, particularly inflammatory disorders.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hematopoietic system, expression of this gene at significantly higher or 5 lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, or cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not 10 having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of 15 potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also 20 used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell 25 types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:11 and may have been publicly available prior to conception of the present invention. 30 Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 852 of SEQ ID NO:11, b is an integer of 15 to 866, where 35 both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:11, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

This gene is expressed primarily in anergic T cells, and to a lesser extent, in
5 other tissues.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune or hematopoietic disorders, particularly inflammatory disorders.
10 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune,
15 hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a
20 sequence shown in SEQ ID NO:41 as residues: Arg-26 to Gln-32.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of
25 potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also
30 used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell
35 types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible

- through sequence databases. Some of these sequences are related to SEQ ID NO:12 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly,
- 5 preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 637 of SEQ ID NO:12, b is an integer of 15 to 651, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where b is greater than or equal to a + 14.
- 10
- FEATURES OF PROTEIN ENCODED BY GENE NO: 3**
- This gene is expressed primarily in spinal cord, and to a lesser extent, in other tissues.
- 15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neural or central nervous system disorders, particularly neurodegenerative disorders. Similarly, polypeptides and antibodies directed to these
- 20 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. neural, spinal cord, and cancerous and wounded tissues) or bodily fluids
- 25 (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:42 as residues: Lys-25 to Ser-33.
- 30 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS,
- 35 psychoses , autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the

developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible

5 through sequence databases. Some of these sequences are related to SEQ ID NO:13 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides

10 comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1322 of SEQ ID NO:13, b is an integer of 15 to 1336, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where b is greater than or equal to a + 14.

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

This gene is expressed primarily in fibrosarcoma, and to a lesser extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as

20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, musculoskeletal disorders, particularly proliferative disorders such as fibrosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)

25 or cell type(s). For a number of disorders of the above tissues or cells, particularly of the musculoskeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.musculoskeletal, and cancerous and wounded tissues) or bodily fluids (e.g.lymph , serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an

30 individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this gene would be useful for the detection, treatment, and/or prevention of various muscle disorders,such

35 as muscular dystrophy, cardiomyopathy, fibroids, myomas, and rhabdomyosarcomas. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide

sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:14 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present

5 invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 571 of SEQ ID NO:14, b is an integer of 15 to 585, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:14, and where

10 b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 5

The gene encoding the disclosed cDNA is believed to reside on chromosome 1.

15 Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in fast growing tissues such as human whole embryo, fetal brain, and cancer tissues, and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as

20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental or proliferative disorders, such as growth deficiencies or tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)

25 or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fast growing tissues such as fetal tissues and cancer tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. proliferative, developmental, and cancerous and wounded tissues) or bodily fluids (e.g. amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or

30 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution within fetal tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein

- may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Alternatively, expression within human fetal brain indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such
- 5 as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of
- 10 developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of
- 15 these sequences are related to SEQ ID NO:15 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the
- 20 general formula of a-b, where a is any integer between 1 to 1130 of SEQ ID NO:15, b is an integer of 15 to 1144, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where b is greater than or equal to a + 14.
- 25
- FEATURES OF PROTEIN ENCODED BY GENE NO: 6**
- This gene is expressed primarily in stromal cells, and to a lesser extent, in other tissues.
- Therefore, polynucleotides and polypeptides of the invention are useful as
- 30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, defects of stromal cell development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
- 35 of the above tissues or cells, particularly of the stromal cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily

fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 5 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in stromal cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product
- 10 may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune
- 15 deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a
- 20 tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:16 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the
- 25 present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1023 of SEQ ID NO:16, b is an integer of 15 to 1037, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID
- 30 NO:16, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

This gene is expressed primarily in cancer tissues, as well as, thyroid, and to

35 a lesser extent in prostate cancer, testes, and macrophage.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, reproductive, endocrine, or immune disorders, particularly tumorigenesis, immuneodeficiencies, bacterial infections, or inflammatory disorders.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in

- 5 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancers and thyroid, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. reproductive, endocrine, immune, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:46 as residues: Met-1 to Gln-7.
- 10

- 15 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cancer and other proliferative disorders. Expression within tumors and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division. Additionally, the expression in hematopoietic cells and tissues indicates that
- 20 this protein may play a role in the proliferation, differentiation, and/or survival of hematopoietic cell lineages. In such an event, this gene may be useful in the treatment of lymphoproliferative disorders, and in the maintenance and differentiation of various hematopoietic lineages from early hematopoietic stem and committed progenitor cells. Similarly, embryonic development also involves decisions involving cell differentiation
- 25 and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Alternatively, the tissue distribution within various endocrine tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and cancers,
- 30 particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancreas (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g., hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-, hypoparathyroidism), hypothalamus, and testes. Moreover, the expression within various reproductive organs indicates that the protein product of this gene may show
- 35 utility in the detection, treatment, and/or prevention of a variety of reproductive disorders, particularly male infertility. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the

above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:17 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically 5 excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 911 of SEQ ID NO:17, b is an integer of 15 to 925, where both a and b correspond to the positions of nucleotide 10 residues shown in SEQ ID NO:17, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

The gene encoding the disclosed cDNA is believed to reside on chromosome 15 12. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 12.

This gene is expressed primarily in brain, reproductive organs, and immune cell/tissues, and to a lesser extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as 20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neuronal, reproductive, or immune and inflammatory diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell 25 type(s). For a number of disorders of the above tissues or cells, particularly of the brain, reproductive organs, and immune cell/tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. neural, reproductive, immune, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal 30 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in brain indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative 35 disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS,

psychoses , autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, the secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological activities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines;

5 immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility);

10 chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behaviour. Also contemplated is the use of the corresponding

15 nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:18 and may have been publicly available prior to conception

20 of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1183 of SEQ ID NO:18, b is an

25 integer of 15 to 1197, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 9

35 This gene is expressed primarily in human tonsils and B-cells from lymphoma patients.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders related to immune system, particularly B-cell lymphoma.

- 5 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types or cell types
- 10 (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:48 as residues: Ser-51 to Leu-60.
- 15

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:19 and may have been publicly available prior to conception of the present invention.

30 Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides

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comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1092 of SEQ ID NO:19, b is an integer of 15 to 1106, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:19, and where b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 10

The gene encoding the disclosed cDNA is believed to reside on chromosome 3. Accordingly, polynucleotides related to this invention are useful as a marker in linkage 10 analysis for chromosome 3.

This gene is expressed primarily in resting T-cells, fetal liver and spleen. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are 15 not limited to, developmental disorders, or disorders related to immune system, particularly immunodeficiencies and inflammatory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of 20 this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. developmental, differentiating, immune, hepatic, and cancerous and wounded tissues) or bodily fluids (e.g. amniotic fluid, lymph, bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene 25 expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in 30 the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, 35 the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel

disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, expression within fetal tissue and other cellular sources marked by

5 proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in

10 cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:20 and may have been publicly available prior to conception of the present

15 invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 918 of SEQ ID NO:20, b is an integer of 15 to

20 932, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

25 The translation product of this gene shares sequence homology with the human TATA-binding protein-associated factor dTAFII250 which is thought to be a general transcriptional activator of RNA polymerase II (See Genbank Accession no.R56493).In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

30 GRPTRPKTPYDESKFYIGCDLCTNWYHGECVGITEKEAKKMDVYICNDCKRA
QEGSSEELYCICRTPYDE SQFYIGCDRCQNWYHGRCVGILQSEAEELIDEYVC
PQCQSTEDAMTVLTPLTEKDYEGLKRVRLSLQAHKM AWPFLEPVDPND
APDYYGVIKEPMDLATMEERVQRRYYEKLTEFVADMTKIFDNCRYYNPSDSPF
YQCAE VLESFFVQKLKGFKASRSHNNKLQSTAS (SEQ ID NO:69).

35 Polynucleotides encoding these polypeptides are also encompassed by the invention.
This gene is expressed primarily in Jurkat T-cells and human Striatum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, disorders of immune or nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, neural, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:50 as residues: Gln-24 to Lys-30, Gly-41 to Ala-46, Ala-97 to Pro-103.

The tissue distribution in human striatum indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the

- expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST
- 5 sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:21 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention
- 10 are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1018 of SEQ ID NO:21, b is an integer of 15 to 1032, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where b is greater than or equal to a + 14.
- 15

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

This gene is expressed primarily in human umbilical vein endothelial cells, breast, and to a lesser extent in placenta.

- 20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, vascular or developmental disorders, particularly those involving the umbilical cord or placenta, in addition to reproductive disorders. Similarly,
- 25 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endothelial system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. endothelial, vascular, reproductive, breast,
- 30 developmental, and cancerous and wounded tissues) or bodily fluids (e.g. amniotic fluid, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 35 The tissue distribution in umbilical cord endothelial cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of cardiovascular disorders, such as atherosclerosis, vasculitis,

microvascular disease, and other related blood vessel disorders. Similarly, expression within embryonic tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders.

- 5 Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide
10 sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:22 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably
15 excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 473 of SEQ ID NO:22, b is an integer of 15 to 487, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 13

This gene is expressed primarily in human brain, fetal liver spleen, dendritic cells, and to a lesser extent in human B-cell lymphoma.

- 25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, neural, immune, or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
30 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous or immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. neural, immune, hematopoietic, hepatic, developmental, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g. lymph,
35 amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an

individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:52 as residues: Met-1 to Pro-10, Pro-19 to Gln-32, Gln-73 to Asp-80.

- The tissue distribution in brain indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Alternatively, the expression within various immune cells, in addition to fetal liver/spleen indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in B-cell lymphoma and dendritic cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:23 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1446 of SEQ ID NO:23, b is an integer of 15 to 1460, where

both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where b is greater than or equal to a + 14.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 14

This gene is expressed primarily in human adult pulmonary tissue, and to a lesser extent in human kidney and messangial cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, cardiovascular disorders, particularly respiratory system disorders, such as emphysema, or kidney disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the respiratory or renal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. pulmonary, cardiovascular, kidney, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, pulmonary surfactant, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:53 as residues: Glu-8 to Val-18.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of respiratory disorders, including emphysema, asthma, or bronchitis. Alternatively, expression in human kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritis, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:24 and may have been publicly available prior to conception of the present invention. Preferably, such related

- polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1084 of
- 5 SEQ ID NO:24, b is an integer of 15 to 1098, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where b is greater than or equal to a + 14.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 15**

This gene is expressed primarily in human cerebellum. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are 15 not limited to, neural or central nervous system disorders, particularly neurodegenerative disorders such as Alzheimers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at 20 significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. neural, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an 25 individual not having the disorder.

The tissue distribution in human cerebrum indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, 30 dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the 35 cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available

and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:25 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

- 5 Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1001 of SEQ ID NO:25, b is an integer of 15 to 1015, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 16

- When tested against K562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon- sensitive responsive element) promoter element. Thus, it is likely that this gene activates leukemia cells through the Jaks-STAT signal transduction pathway. ISRE is a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in human endothelial cells and human stromal endometrial fibroblasts.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, integumentary disorders, particularly endothelial or fibroblast related disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the integumentary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.integumentary, endothelial, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not

having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:55 as residues: Glu-35 to Gln-40.

The tissue distribution in endothelial tissues and fibroblasts, combined with the observed ISRE biological activity indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e. wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, athletes foot, and ringworm). Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:26 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1183 of SEQ ID NO:26, b is an integer of 15 to 1197, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 17

The translation product of this gene shares sequence homology with ATP/GTP binding site motif A of *Saccharomyces cerevisiae* (See Genbank Accession No.gnl|PIDle217937) which is thought to be important in the regulation of various cellular processes, including transcription of important genes, in addition to signal transduction pathways. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:
TKFVQCPDGELQKRKEVVHTVSLHEIDVINSRTQGFLALFSGDTGEIKSEVRE
QINAKVAEWREEGKAEIIPGVLFIDEVHMLDIESFSFLNRALESDMAPVLIMATN

RGITRIRGTSYQSPH GIPIDLLDRLLIVSTTPYSEKDTKQILRIRCEEEDVEM
SEDAYTVLTRIGLETSLRYAIQLITAASLVCR KRKGTEVQVDDIKRVYSLFL
DESRSTQYMKEYQDAFLFNELKGETMDTS (SEQ ID NO:70), VVHTVSLH
EIDVINSRTQGFLALF (SEQ ID NO:71), PGVLFIDEVHMLDIE (SEQ ID NO:72), or

- 5 EEGKAEI (SEQ ID NO:73). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in human adult testis, and to a lesser extent, in activated T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, male reproductive, endocrine, or immune disorders, particularly male infertility resulting from autoimmunity. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
15 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. reproductive, endocrine, immune, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal
20 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:56 as residues: Arg-34 to His-42, Pro-59 to Gln-67, Arg-112 to Thr-117, Glu-134 to Gln-139, Glu-156 to Ser-161.

25 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of a variety of male reproductive disorders, particularly male infertility. Similarly, the tissue distribution in testes indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and
30 cancers, particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancreas (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g., hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-, hypoparathyroidism), hypothalamus, and testes. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy
35 targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:27 and may have been publicly available

- prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the
- 5 general formula of a-b, where a is any integer between 1 to 988 of SEQ ID NO:27, b is an integer of 15 to 1002, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where b is greater than or equal to a + 14.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 18**

The gene encoding the disclosed cDNA is believed to reside on chromosome 1. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 1.

- This gene is expressed primarily in human placenta.
- 15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, reproductive or developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
- 20 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly reproductive disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, developmental, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid)
- 25 or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, treatment, or prevention of
- 30 various reproductive, developmental, or congenital disorders, particularly Tay-Sachs disease, phenylketonuria, galactosemia, hyperlipidemias, porphyrias, and Hurler's syndrome. Alternatively, expression within placental tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and
- 35 other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in

- cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:28 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of 10 a-b, where a is any integer between 1 to 1313 of SEQ ID NO:28, b is an integer of 15 to 1327, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:28, and where b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 19

The gene encoding the disclosed cDNA is believed to reside on chromosome 15. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 15.

This gene is expressed primarily in human fetal brain, and to a lesser extent in 20 pineal gland, prostate, and thyroid.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, endocrine, reproductive, neural, or developmental disorders. Similarly, 25 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.endocrine, reproductive, neural, developmental, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a 30 sequence shown in SEQ ID NO:58 as residues: Val-32 to Asn-40, Gly-59 to Gly-65.

The tissue distribution amongst various endocrine tissues indicates that 35 polynucleotides and polypeptides corresponding to this gene are useful for the

detection, treatment, and/or prevention of various endocrine disorders and cancers, particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancreas (e.g. diabetes mellitus), adrenal cortex, ovaries, pituitary (e.g., hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-, hypoparathyroidism), hypothalamus, and testes. Alternatively, the tissue distribution in fetal brain indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:29 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 654 of SEQ ID NO:29, b is an integer of 15 to 668, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

This gene is expressed primarily in Merkel cells. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, integumentary disorders or diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or integumentary system,

- expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.integumentary, immune, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- The tissue distribution in Merkel cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e.wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, althletes foot, and ringworm). Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:30 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.
- Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1229 of SEQ ID NO:30, b is an integer of 15 to 1243, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.
- 30

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

- This gene is expressed primarily in Merkel cells.
- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, integumentary diorders, particularly in the diagnosis, treatment, or

- prevention of melanoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and integumentary systems, expression of 5 this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. integumentary, immune, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily 10 fluid from an individual not having the disorder.

The tissue distribution in Merkel cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors 15 (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e. wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, 20 pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, athlete's foot, and ringworm). Many polynucleotide sequences, such as EST sequences, are publicly 25 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:31 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more 30 polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1039 of SEQ ID NO:31, b is an integer of 15 to 1053, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:31, and where b is greater than or equal to a + 14.

This gene is expressed primarily in Merkel cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, integumentary or immune system diseases and disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and integumentary systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, integumentary, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:61 as residues: Ile-74 to His-79.

The tissue distribution in Merkel cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e. wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, athletes foot, and ringworm). Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:32 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1000 of SEQ ID NO:32, b is an integer of 15

to 1014, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to a + 14.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 23

This gene is expressed primarily in fetal liver spleen, and to a lesser extent in, bone marrow stromal cells and Jurket membrane bound polysomes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

- 10 biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental or immune disorders, particularly immunodeficiencies or inflammatory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above
15 tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, developmental, hepatic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, bile, synovial fluid and spinal fluid) or another tissue or cell sample taken from an
20 individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:62 as residues: Leu-23 to Gln-29, Glu-33 to Ile-44.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of
25 neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Similarly, expression within fetal tissues and
30 other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development
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also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets

5 for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:33 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related

10 sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1359 of SEQ ID NO:33, b is an integer of 15 to 1373, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and where b is greater than or equal to a

15 + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

The translation product of this gene shares sequence homology with cni gene product (Cornichon protein) of Drosophila melanogaster which is involved in signal processing during development (See Genbank Accession No.gil2460430).In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: SRPVMSGPGLYDPTTIMNADILAYCQKEGW (SEQ ID NO:74), FFCV MFLCAAEWLTLGLNMPLLAYHIWRYM (SEQ ID NO:75), WHIIAFDELKTD 25 YKNPIDQCNTLNPLVLPEYLIHA (SEQ ID NO:76), GSPGCRNSATAKAPRS SSPA (SEQ ID NO:77), MAFTFAAFCYM (SEQ ID NO:78), or GMIYVLVSS (SEQ ID NO:79). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in melanocytes.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, integumentary disorders, particularly melanocytoma and other cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in

35 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be

routinely detected in certain tissues or cell types (e.g. melanocytes, immune, integumentary, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

- 5 expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:63 as residues: Leu-34 to Gln-44.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of
10 various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e. wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, uticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum
20 contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, athletes foot, and ringworm). Based upon the homology to the Cornichun protein, it may be inferred that the protein product of this gene is useful for the detection, treatment, and/or prevention of a variety of proliferative disorders, particularly cancers, ulcers, or tumors. Protein, as well as, antibodies directed against the protein may show utility as a
25 tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:34 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the
30 present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1390 of SEQ ID NO:34, b is an integer of 15 to 1404, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID
35 NO:34, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

- When tested against K562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon-sensitive responsive element) 5 promoter element. Thus, it is likely that this gene activates leukemia cells through the Jak-STAT signal transduction pathway. ISRE is a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the 10 ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in fetal tissue, and to a lesser extent, in human B cell lymphoma.

- Therefore, polynucleotides and polypeptides of the invention are useful as 15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, developmental or immune disorders, particularly B cell diseases, such as lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) 20 or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. developmental, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue 25 or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of 30 immune system disorders. Expression of this gene product in B-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by 35 boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune

deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Similarly, expression within fetal tissue and other cellular sources marked by proliferating cells, combined with the detected ISRE biological activity, indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:35 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1079 of SEQ ID NO:35, b is an integer of 15 to 1093, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 26

The translation product of this gene shares sequence homology with human complement decay-accelerating factor (DAF) (See Genbank Accession No. gil1857867). DAF is believed to play an important role in the regulation of the complement cascade, specifically this protein recognizes c4b and c3b fragments that condense with cell-surface hydroxyl or amino groups when nascent c4b and c3b are locally generated during c4 and c3 activation. interaction of daf with cell-associated c4b and c3b polypeptides interferes with their ability to catalyze the conversion of c2 and factor b to enzymatically active c2a and bb and thereby prevents the formation of c4b2a and c3bbb, the amplification convertases of the complement cascade. In addition, mutation of DAF has been found to lead to the Cromer blood group system which consists of at least seven high-incidence (cr(a), tc(a), dr(a), es(a), wes(b), umc, and ifc)

- and low-incidence (tc(b), tc(c), and wes(a)) antigens that reside on DAF. In the cromer phenotypes dr(a-) and in ab there is reduced or absent expression of DAF, respectively. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: NSFFFPCCFRYKLFGSTSSFCLISGSSVQWSDPXPECRGKS (SEQ 5 ID NO:80). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 1. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 1.
- This gene is expressed primarily in activated human neutrophils.
- 10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune or hematopoietic disorders, particularly neutropenia, in addition to disorders related to the complement or neural system. Similarly, polypeptides and 15 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hemopoietic, complement, or neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, neural and 20 cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 25 The tissue distribution in neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in tonsils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This 30 gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including 35 arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells

- and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Similarly, the tissue distribution in neutrophils combined with the homology to the DAF protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection, treatment, or prevention of a variety of blood disorders, particularly complement disorders, or disorders related to blood group antigens, such as the Cromer blood group system (i.e. transfusions, etc.) Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:36 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 404 of SEQ ID NO:36, b is an integer of 15 to 418, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 27

- When tested against K562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon- sensitive responsive element) pathway. Thus, it is likely that this gene activates leukemia cells through the Jaks-STAT signal transduction pathway. ISRE is a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in neutrophils.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions:immune disorders, particularly neutropenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above

- tissues or cells, particularly of the immune or hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or
- 5 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:66 as residues: Asp-45 to Thr-50.

The tissue distribution in neutrophils combined with the detected ISRE

10 biological activity indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be

15 involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune

20 deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a

25 tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:37 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the

30 present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1028 of SEQ ID NO:37, b is an integer of 15 to 1042, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID

35 NO:37, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 28

- When tested against K-562 cell lines, supernatants removed from cells containing this gene activated the ISRE (interferon- sensitive responsive element) promoter element. Thus, it is likely that this gene activates leukemia cells through the Jaks-STAT signal transduction pathway ISRE is a promoter element found upstream in many genes which are involved in the Jaks-STAT pathway. The Jaks-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in activated T-cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune or hematopoietic disorders, particularly immunodeficiencies such as AIDS, or inflammatory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in T-cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel

disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:38 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 784 of SEQ ID NO:38, b is an integer of 15 to 798, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:38, and where b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed primarily in neutrophils. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions, which include, but are not limited to, immune or hematopoietic disorders, particularly neutropenia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hemopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of

potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin,

5 the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of

10 various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:39 and

15 may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is

20 any integer between 1 to 1016 of SEQ ID NO:39, b is an integer of 15 to 1030, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:39, and where b is greater than or equal to a + 14.

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	NT SEQ ID Total NO: NT Seq. X	5' NT of Clone Seq.	3' NT of Clone Seq.	S' NT of AA SEQ ID of Signal NO: Sig Pep Y	First AA of AA SEQ ID of Signal NO: Sig Pep Y	Last AA of AA SEQ ID of Signal NO: Sig Pep Y	First AA of AA SEQ ID of Signal NO: Sig Pep Y	Last AA of AA SEQ ID of Signal NO: Sig Pep Y	AA Secreted Portion	Last AA of AA SEQ ID of Signal NO: Sig Pep Y	AA Secreted Portion	Last AA of AA SEQ ID of Signal NO: Sig Pep Y	AA Secreted Portion
1	HSAXS66	209197 08/08/97	Uni-ZAP XR 08/08/97	11	866	1	866	102	102	40	1	24	25	36	
2	HSAYL90	209197 08/08/97	Uni-ZAP XR 08/08/97	12	651	1	651	188	188	41	1	21	22	32	
3	HSDIT06	209197 08/08/97	Uni-ZAP XR 08/08/97	13	1336	1	1336	123	123	42	1	18	19	91	
4	HSFAL43	209197 08/08/97	Uni-ZAP XR 08/08/97	14	585	1	585	123	123	43	1	30	31	32	
5	HSKEI54	209197 08/08/97	Uni-ZAP XR 08/08/97	15	1144	175	1144	316	316	44	1	36	37	52	
6	HSQBE28	209197 08/08/97	Uni-ZAP XR 08/08/97	16	1037	229	1037	317	317	45	1	17	18	25	
7	HTEAN76	209197 08/08/97	Uni-ZAP XR 08/08/97	17	925	156	925	260	260	46	1	31	32	37	

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	NT SEQ ID NO: NT Seq. X	NT SEQ ID NO: NT Seq. X	5' NT of Clone Seq. Start Signal Codon Pep	5' NT of AA of ID NO: Sig Pep	First AA of AA Sig Pep	Last AA of AA Sig Pep	First AA of AA Sig Pep	Last AA of AA Sig Pep	Last AA of AA Sig Pep
8	HTNAG39	209197 08/08/97	pBluescript SK-	18 1197	403 1191	468 468	468 47	1 1	45 39	46 40	70
9	HTODL90	209197 08/08/97	Uni-ZAP XR	19 1106	1 1106	925 925	925 48	1 1	39 26	40 27	60
10	HTWDC20	209197 08/08/97	pSport1	20 932	1 932	156 156	156 49	1 1	26 26	27 27	39
11	HUFAT34	209197 08/08/97	pSport1	21 1032	1 1032	32 32	32 50	1 1	22 16	23 17	103
12	HUSGX69	209197 08/08/97	pSport1	22 487	1 487	243 243	243 51	1 1	16 16	17 17	22
13	HAICJ23	209197 08/08/97	Uni-ZAP XR	23 1460	1 1460	189 189	189 52	1 1	47 47	48 48	85
14	HAPOF67	209197 08/08/97	Uni-ZAP XR	24 1098	1 1098	78 78	78 53	1 1	47 47	48 48	73
15	HCEBR71	209197 08/08/97	Uni-ZAP XR	25 1015	1 1015	102 102	102 54	1 1	17 17	18 18	35

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	NT SEQ ID Total NO: NT Seq. X	5' NT of Clone Seq. Start Seq.	3' NT of AA of Signal NO:	5' NT of AA SEQ ID of AA of Signal NO:	First AA of AA Sig Pep	Last AA of AA Sig Pep	First AA of AA Secreted Portion	Last AA of AA Secreted Portion
				Clone Seq.	Codon Pep	Pep Y				
16	HE8DG53	209197 08/08/97	Uni-ZAP XR	26	1197	307	1197	350	55	1
17	HFSAY85	209197 08/08/97	Uni-ZAP XR	27	1002	457	1002	295	56	1
18	HHEDD4I	209197 08/08/97	pCMV Sport 3.0	28	1327	154	1327	442	57	1
19	HKCSO46	209197 08/08/97	pBluescript	29	668	20	668	217	58	1
20	HKGAV60	209197 08/08/97	pSport I	30	1243	1	1243	192	59	1
21	HKGDJ35	209197 08/08/97	pSport I	31	1053	1	1053	238	60	1
22	HKGDJ66	209197 08/08/97	pSport I	32	1014	1	1014	215	61	1
23	HMCDK27	209197 08/08/97	Uni-ZAP XR	33	1373	1	969	33	33	62

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	NT SEQ ID Total NO: NT Seq. X	NT of 3' NT of 5' NT	Clone Clone of AA of SEQ First AA	5' NT of AA SEQ ID of AA of SEQ First AA	Last AA of SEQ ID of AA of SEQ First AA	Last AA of AA of SEQ ID of AA of SEQ First AA
				Seq. Start Codon Pep	Signal NO: Sig Pep	Secreted Y Pep	Portion of ORF	Last AA of AA of SEQ ID of AA of SEQ First AA
24	HMCDX48	209197 08/08/97	Uni-ZAP XR 34	1404 1	1403 63	63 63	1 30	31 144
25	HMIAS24	209197 08/08/97	Uni-ZAP XR 35	1093 1	1093 178	178 64	1 42	43 44
26	HNFEGL1	209197 08/08/97	Uni-ZAP XR 36	418 1	418 251	251 65	1 31	32 47
27	HNGEPO9	209197 08/08/97	Uni-ZAP XR 37	1042 1	1042 72	72 66	1 15	16 82
28	HTXKK52	209197 08/08/97	Uni-ZAP XR 38	798 1	798 81	81 67	1 30	31 48
29	HNCPJP90	209197 08/08/97	Uni-ZAP XR 39	1030 1	1030 157	157 68	1 14	15 94

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification , such as multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988).
Polypeptides of the invention also can be purified from natural or recombinant sources
10 using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, Virus Res. 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, Nucleic Acids Res. 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, supra.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide
25 was analyzed by a computer program called SignalP (Henrik Nielsen et al., Protein Engineering 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results
30 shown in Table 1.

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., + or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in
35 some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

10 **Polynucleotide and Polypeptide Variants**

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

15 By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

20 As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization

Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the lenght of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is becuase the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignement of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequnce are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query

amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions,

- 5 interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by deposited DNA clone can be

- 10 determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and
15 subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window
20 Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity.

- 25 For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of
30 the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are
35 considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the subject sequence.

- For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired
- 5 residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence.
- 10 This time the deletions are internal deletions so there are no residues at the N- or C- termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query
- 15 sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or

20 activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in

25 the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (*Genes II*, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level.

30 Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., *J. Biol. Chem.* 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after

deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1 α . They used random mutagenesis to generate over 3,500 individual IL-1 α mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham 5 and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the 10 protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues 15 Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, 20 where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino 25 acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins 30 with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt,

5 and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000

10 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900,

15 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, or 2001 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger

20 or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity. More preferably, these polynucleotides can be used as probes or primers as discussed herein.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-

- 60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred.
- 5 Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions.

10 Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

15 Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

20

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983).)

30 Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to 35 about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow, M. et al., *Proc. Natl. Acad. Sci. USA* 82:910-914; and Bittle, F. J. et al., *J. Gen. Virol.* 66:2347-2354 (1985).) A preferred immunogenic epitope includes 5 the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a 10 denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')2 fragments) which are capable of specifically binding to protein. Fab and F(ab')2 fragments lack the Fc fragment of intact antibody, clear more rapidly from 15 the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., *J. Nucl. Med.* 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and 20 humanized antibodies.

20

Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the 25 polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention 30 include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

Moreover, fusion proteins may also be engineered to improve characteristics of 35 the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the

polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

- Moreover, polypeptides of the present invention, including fragments, and
- 5 specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of
- 10 mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)
- 15 Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively,
- 20 deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D.
- 25 Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide,

30 such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

- Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., *Basic Methods*
- 5 In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography,

10 phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

30 **Uses of the Polynucleotides**

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat

polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the 10 polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include *in situ* hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome 15 specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence *in situ* hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., 20 "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides 25 correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage 30 analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library).) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease 35 could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined.

First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the

5 mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected
10 individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene
15 expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science
20 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model
25 systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the
30 present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of
35 restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying

personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

- 5 The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set
10 of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as
15 tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more
20 restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of
25 unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

- 30 In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using
35 DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

- A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., *J. Cell. Biol.* 101:976-985 (1985); Jalkanen, M., et al., *J. Cell. Biol.* 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.
- In addition to assaying secreted protein levels in a biological sample, proteins can also be detected *in vivo* by imaging. Antibody labels or markers for *in vivo* imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.
- A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, 131I, 112In, 99mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of 99mTc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. *In vivo* tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in *Tumor Imaging: The Radiochemical Detection of Cancer*, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

- 5 Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S 10 for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).
- 15 Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).
- 20 At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the 25 polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

- The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the

- proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders
- 5 may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotide or polypeptide of the present invention may be useful in

10 treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to:

15 blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

20 Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet

25 disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

30 A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the

35 present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

- Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis,
- 5 Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.
- 10 Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.
- A polynucleotide or polypeptide of the present invention may also be used to
- 15 treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that inhibits
- 20 an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.
- Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may inhibit the proliferation and differentiation of cells involved in an inflammatory
- 25 response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel
- 30 disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect

interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

- For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.
- 10 Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.
- 15 Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary

- 20 Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

- 25 A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the
- 30 polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

- Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following
- 35 DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes

- Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps,
- 5 10 Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.
- Similarly, bacterial or fungal agents that can cause disease or symptoms and that
- 15 20 25 30 35 can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Nocardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Menigococcal), Pasteurellacea Infections (e.g., Actinobacillus, Haemophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, 5 Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide 10 of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide 15 of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

20 A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal 25 disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and 30 skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase 35 regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue

regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate 5 nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized 10 neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

15 **Chemotaxis**

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of 20 hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to 25 tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present 30 invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

35 A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit

(antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the
5 polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology
1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can
10 be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed
15 polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a
20 labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate
25 compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The
30 antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the
35 polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

- Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying 5 agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity , and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

- 10 A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.
- A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, 15 skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.
- 20 A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, caricadic rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.
- 25 A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

30 Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

- 35 Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of

positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

- Also preferred is a nucleic acid molecule wherein said sequence of contiguous
5 nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of
positions beginning with the nucleotide at about the position of the 5' Nucleotide of the
Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of
the Clone Sequence as defined for SEQ ID NO:X in Table 1.

- Similarly preferred is a nucleic acid molecule wherein said sequence of
10 contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the
range of positions beginning with the nucleotide at about the position of the 5'
Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide
at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID
NO:X in Table 1.

- 15 Also preferred is an isolated nucleic acid molecule comprising a nucleotide
sequence which is at least 95% identical to a sequence of at least about 150 contiguous
nucleotides in the nucleotide sequence of SEQ ID NO:X.

- Further preferred is an isolated nucleic acid molecule comprising a nucleotide
sequence which is at least 95% identical to a sequence of at least about 500 contiguous
20 nucleotides in the nucleotide sequence of SEQ ID NO:X.

- A further preferred embodiment is a nucleic acid molecule comprising a
nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ
ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the
First Amino Acid of the Signal Peptide and ending with the nucleotide at about the
25 position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in
Table 1.

- A further preferred embodiment is an isolated nucleic acid molecule comprising
a nucleotide sequence which is at least 95% identical to the complete nucleotide
sequence of SEQ ID NO:X.

- 30 Also preferred is an isolated nucleic acid molecule which hybridizes under
stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid
molecule which hybridizes does not hybridize under stringent hybridization conditions
to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or
of only T residues.

- 35 Also preferred is a composition of matter comprising a DNA molecule which
comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1,
which DNA molecule is contained in the material deposited with the American Type

Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

- Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.
- 5

- Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete 10 open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

- A further preferred embodiment is an isolated nucleic acid molecule comprising 15 a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

- 20 A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone
25 identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% 30 identical to said selected sequence.

- Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of 35 comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

15 Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone 20 identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and 25 contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA 30 clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA 35 clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in
5 Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as
10 defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at
15 least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method
20 comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino
25 acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an
30 amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is
35 performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide 5 comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

10 Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

15 Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid 20 sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human 25 cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an 30 individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of 35 illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

5 Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For
10 example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
15	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSport 2.0	pCMVSport 2.0
	pCMVSport 3.0	pCMVSport 3.0
20	pCR®2.1	pCR®2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128,256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS.
25
30 The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.
35 Vectors pSport1, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain

- DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR®2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P - γ -ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction
5 is carried out under routine conditions, for instance, in 25 µl of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl₂, 0.01% (w/v) gelatin, 20 µM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are
10 performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding
15 portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids
20 Res. 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the
25 desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged
30 RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

35 This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is

used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

5

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X.,

10 according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by,

15 among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is
20 then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are

25 mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' 30 end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual 35 chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on

either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

5 **Example 5: Bacterial Expression of a Polypeptide**

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as
10 BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^R), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.
15

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses
20 the lacI repressor and also confers kanamycin resistance (Kan^R). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml).
25 The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D. ⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

30 Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrolo-tri-acetic acid ("Ni-NTA") affinity resin column (available from
35 QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high

affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed 5 with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the 10 protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After 15 renaturation the proteins are eluted by the addition of 250 mM immidazole. Immidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a 20 neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

25 DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or 30 Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

35 **Example 6: Purification of a Polypeptide from an Inclusion Body**

The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem

columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column 5 volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above 10 refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

15 **Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System**

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide 20 into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient 25 polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak Drosophila promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated 30 homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such 35 as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., Virology 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the 35 AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring

signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures,"

- 5 Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

- 10 The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue

- 15 (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

- 20 Five µg of a plasmid containing the polynucleotide is co-transfected with 1.0 µg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One µg of BaculoGold™ virus DNA and 5 µg of the plasmid are mixed in a sterile well of a 25 microtiter plate containing 50 µl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 µl Lipofectin plus 90 µl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then 30 incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

- 35 After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture

and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 µCi of ³⁵S-methionine and 5 µCi ³⁵S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

20 **Example 8: Expression of a Polypeptide in Mammalian Cells**

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

30 Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSport 2.0, and pCMVSport 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, 35 Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

- 5 The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a
- 10 chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.
- 15

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

- 5 Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μ g of the expression plasmid pC6 is cotransfected with 0.5 μ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that
- 10 confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri
- 15 dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 -
- 20 200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins.

25 These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the

30 polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion

35 proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

- 5 For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with 10 BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that 15 the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

- If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a 15 heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

GGGATCCGGAGCCAAATCTTCTGACAAAACCTCACACATGCCACCACGTGCC
CAGCACCTGAATTGAGGGTGACCGTCAGTCTCCTCTCCCCCAAACCC
20 CAAGGACACCCCTCATGATCTCCCGACTCCTGAGGTACATGCGTGGTGGT
GGACGTAAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTCACCGCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTCAAGGTCTCCAACAAAGCCCTCCAACCCCC
25 ATCGAGAAAACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCAACAGGT
GTACACCCCTGCCCATCCGGATGAGCTGACCAAGAACCAAGGTACGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATGCCGTGGAGTGGGA
GAGCAATGGCAGCCGGAGAACAAACTACAAGACCACGCCTCCGTGCTGG
ACTCCGACGGCTCCTCTTCTACAGCAAGCTACCCGTGGACAAGAGCA
30 GGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAAACCAACTACACGCAGAAGAGCCTCTCCGTCTCCGGTAAATGAGTGC
GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

Example 10: Production of an Antibody from a Polypeptide

- 35 The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera

containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

- 5 In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., *Nature* 256:495 (1975); Köhler et al., *Eur. J. Immunol.* 6:511 (1976); Köhler et al., *Eur. J. Immunol.* 6:292 (1976); Hammerling et al., in: *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

- The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (*Gastroenterology* 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

- 25 Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

- It will be appreciated that Fab and F(ab')2 and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). Alternatively, 5 secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies 10 described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulian et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 15 (1985).)

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be 20 tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) 25 and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel!). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

30 Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

35 The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in

- Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a 5 control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of 10 cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM 15 with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl₂ (anhyd); 0.00130 mg/L CuSO₄·5H₂O; 0.050 mg/L of Fe(NO₃)₃·9H₂O; 0.417 mg/L of FeSO₄·7H₂O; 311.80 mg/L of KCl; 28.64 mg/L of MgCl₂; 48.84 mg/L of MgSO₄; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO₃; 62.50 mg/L of NaH₂PO₄·H₂O; 71.02 mg/L of Na₂HPO₄; .4320 mg/L of ZnSO₄·7H₂O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of 20 Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitic Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml 25 of L-Asparagine-H₂O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H₂O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H₂O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H₂O; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 35 0.680 mg/L of Vitamin B₁₂; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine;

- 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-10, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN- α , IFN- γ , and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>Ligand</u>	<u>tyk2</u>	<u>JAKs</u>	<u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>	<u>STATs</u>	<u>GAS(elements) or ISRE</u>
<u>IFN family</u>								
5	IFN-a/B	+	+	-	-	-	1,2,3	ISRE
	IFN-g		+	+	-	-	1	GAS (IRF1>Lys6>IFP)
	Il-10	+	?	?	-	-	1,3	
<u>gp130 family</u>								
10	IL-6 (Pleiotrophic)	+	+	+	?	?	1,3	GAS (IRF1>Lys6>IFP)
	Il-11(Pleiotrophic)	?	+	?	?	?	1,3	
	OnM(Pleiotrophic)	?	+	+	?	?	1,3	
	LIF(Pleiotrophic)	?	+	+	?	?	1,3	
15	CNTF(Pleiotrophic)	-/+	+	+	?	?	1,3	
	G-CSF(Pleiotrophic)	?	+	?	?	?	1,3	
	IL-12(Pleiotrophic)	+	-	+	+	+	1,3	
<u>g-C family</u>								
20	IL-2 (lymphocytes)	-	+	-	+	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	+	6	GAS (IRF1 = IFP >>Ly6)(IgH)
	IL-7 (lymphocytes)	-	+	-	+	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	?	6	GAS
	IL-15	?	+	?	+	+	5	GAS
<u>gp140 family</u>								
	IL-3 (myeloid)	-	-	+	-	-	5	GAS (IRF1>IFP>>Ly6)
	IL-5 (myeloid)	-	-	+	-	-	5	GAS
30	GM-CSF (myeloid)	-	-	+	-	-	5	GAS
<u>Growth hormone family</u>								
	GH	?	-	+	-	-	5	
	PRL	?	+/-	+	-	-	1,3,5	
35	EPO	?	-	+	-	-	5	GAS(B-CAS>IRF1=IFP>>Ly6)
<u>Receptor Tyrosine Kinases</u>								
	EGF	?	+	+	-	-	1,3	GAS (IRF1)
	PDGF	?	+	+	-	-	1,3	
40	CSF-1	?	+	+	-	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., *Immunity* 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5':GCGCCTCGAGATTCCCCGAAATCTAGATTCCCCGAAATGATTCCCCG
10 AAATGATTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5':CTCGAGATTCCCCGAAATCTAGATTCCCCGAAATGATTCCCCGAAATG
20 ATTTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCGGCCC
CTAACTCCGCCCATCCGCCCTAACTCCGCCAGTCCGCCATTCTCCGC
CCCATGGCTGACTAATTTTTATTATGCAGAGGCCGAGGCCCTCGGC
CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTGAGGCCCTAGGCTTT
TGCAAAAAGCTT:3' (SEQ ID NO:5)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, 30 alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS:SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

- 5 Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules
10 containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-
15 2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Rch (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

Example 13: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors,
20 such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jak-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and
25 Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately
30 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to
35 generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies)

with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final

- 5 concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Genticin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

- 10 On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

- 15 Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100,000 cells per well).

- 20 After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

- 25 The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

- 30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells. Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the 5 Jak-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

To transiently transfet U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with 10 PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM 15 KCl, 375 uM Na₂HPO₄.7H₂O, 1 mM MgCl₂, and 675 uM CaCl₂. Incubate at 37°C for 45 min.

Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 20 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the 30 protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are 35 activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon

activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or

5 differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

10 The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCGG -3' (SEQ ID NO:6)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

15 Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes Xhol/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

20 To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker)
25 containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

30 Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

35 To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS

(Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

- The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count
5 the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR
10 can be used, such as 50 ng/ml of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

Example 16: High-Throughput Screening Assay for T-cell Activity

15 NF- κ B (Nuclear Factor κ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- κ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF-
20 κ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κ B is retained in the cytoplasm with I- κ B (Inhibitor κ B). However, upon stimulation, I- κ B is phosphorylated and degraded, causing NF- κ B to shuttle to the nucleus, thereby activating transcription of target
25 genes. Target genes activated by NF- κ B include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- κ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- κ B would be useful in treating
30 diseases. For example, inhibitors of NF- κ B could be used to treat those diseases related to the acute or chronic activation of NF- κ B, such as rheumatoid arthritis.

- To construct a vector containing the NF- κ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- κ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:
- 5 5':GCGGCCTCGAGGGACTTCCCGGGACTTCCGGGACTTCCGGAC
TTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)
- The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:
- 5':GCGGCAAGCTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)
- 10 PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene) Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:
- 15 5':CTCGAGGGACTTCCCGGGACTTCCGGGACTTCCGGACTTCC
ATCTGCCATCTCAATTAGTCAGCAACCATACTCCGCCCTAACTCCGCCA
TCCCGCCCTAACTCCGCCAGTCCGCCATTCTCCGCCCATGGCTGACT
AATTTTTTTATTTATGCAGAGGCCAGGCCCTCGGCCTTGAGCTATT
- 20 CAGAAGTAGTGAGGAGGCTTTGGAGGCCTAGGCTTTGCAAAAAGCTT:
3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2-promoter plasmid (Clontech) with this NF- κ B/SV40 fragment using XhoI and HindIII.

25 However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- κ B/SV40/SEAP cassette is removed from the above NF- κ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the

30 NF- κ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF- κ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described

in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

5 As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

10 Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 µl of 2.5x dilution buffer into Optiplates containing 35 µl of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

15 Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 µl Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 µl Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

20 Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25

28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is

incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10⁶ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml

5 fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension.

The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10⁶ cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

10 For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and
15 (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca⁺⁺ concentration.

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

20 The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In
25 addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the
30 cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

35 Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating

tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

- Seed target cells (e.g., primary keratinocytes) at a density of approximately
- 5 25,000 cells per well in a 96 well Loprodynne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or
- 10 10% Matrigel purchased from Becton Dickinson (Bedford,MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford,MA) are
- 15 used to cover the Loprodynne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

- To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodynne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20
- 20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for
- 25 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after detergent solubilization for 5 minutes, is removed and
- 30 centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

- Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a
- 35 biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and

PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂₊ (5mM

- 5 ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently and preincubate the reaction mix at 30°C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

- 10 The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide.

- 15 Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as above.

- 20 Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

25 **Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity**

- As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase, Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C until use.

5 A431 cells are seeded at 20,000/well in a 96-well Loprodyn filterplate and
10 cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

15 After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with
20 Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

25 RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in
30 SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTHERM Polymerase. (Epicentre Technologies).
35 The intron-exon borders of selected exons is also determined and genomic PCR

products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products are cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenin-deoxy-uridine 5'-triphosphate (Boehringer Manheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

25

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

- The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to
- 5 validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

- Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove
- 10 unbounded conjugate.

- Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on
- 15 the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

- The secreted polypeptide composition will be formulated and dosed in a fashion
- 20 consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

- 25 As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 µg/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If
- 30 given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 µg/kg/hour to about 50 µg/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending
- 35 on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracistemally, intravaginally,

- intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes 5 of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

- The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules.
- 10 Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2-hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D-(-)-3-hydroxybutyric 15 acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008;
- 20 U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

- For parenteral administration, in one embodiment, the secreted polypeptide is 25 formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are 30 known to be deleterious to polypeptides.

- Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood 35 of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

- The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as
- 5 ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose,
- 10 manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of

15 about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed

20 into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials

25 are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical

30 compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

35

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form.

Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

- 5 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the 10 polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

Antisense technology is used to inhibit production of a polypeptide of the 15 present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

- For example, a patient diagnosed with abnormally increased levels of a 20 polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

Example 26: Method of Treatment Using Gene Therapy

One method of gene therapy transplants fibroblasts, which are capable of 25 expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 30 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

- At this time, fresh media is added and subsequently changed every several days. 35 After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

5 The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

10 The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

15 Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

20 The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

25 It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

30 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other

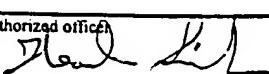
disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties.

123

Applicant's or agent's file reference number	PZ015PCT	International applicant No. Unassigned	137709
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 45, line N/A	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet	
Name of depositary institution American Type Culture Collection	
Address of depositary institution (<i>including postal code and country</i>) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit	August 8, 1997
Accession Number	209197
C. ADDITIONAL INDICATIONS (<i>leave blank if not applicable</i>) This information is continued on an additional sheet	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (<i>if the indications are not for all designated States</i>)	
E. SEPARATE FURNISHING OF INDICATIONS (<i>leave blank if not applicable</i>) The indications listed below will be submitted to the International Bureau later (<i>specify the general nature of the indications, e.g., "Accession Number of Deposit"</i>)	
For receiving Office use only	
<input checked="" type="checkbox"/> This sheet was received with the international application	
Authorized officer 	
For International Bureau use only	
<input type="checkbox"/> This sheet was received by the International Bureau on _____	
Authorized officer	

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

- (a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;
- (e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;
- (f) a polynucleotide which is a variant of SEQ ID NO:X;
- (g) a polynucleotide which is an allelic variant of SEQ ID NO:X;
- (h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;
- (i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15. A method of making an isolated polypeptide comprising:
(a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
(b) recovering said polypeptide.

16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:
(a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and
(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- (a) contacting the polypeptide of claim 11 with a binding partner; and
- (b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
- (b) isolating the supernatant;
- (c) detecting an activity in a biological assay; and
- (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.

<110> Rosen
et al.
Human Genome Sciences, Inc.

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gacgggtct tgctctgttg cccaggctgg agtgcataatgg cgcaatctca gctcactgca	660
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cagctgggtgg gcccaggatgg cmaagggtca tagtttata tcccttgagc taggctgttg	960
ctgaggttga ttcaacatcc cagctccatc caacaacaaa aattctaaatg ctccccccta	1020
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gaaccacagg gctcagaaca ggaaggagct tctttctgca gagctgatc ctggaaagcc	1140
accagcactc caccttctgc ccagaaatgtt gattcgtca atagctgtatc aggaaaagca	1200
acctgcaaactt attaggaaga aggagaaaaaa taattcagag gtgtatgatc cacctccaaat	1260
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aaaaaaaaaa actcgaa 1336

<210> 14
<211> 585
<212> DNA
<213> Homo sapiens

<400> 14
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aggaaggaca ctacaccaca aacatttaa ggacagaatc tgaagtattt gtcaacttag 120
tgatggtgca gggctctggt ggtacctgtt taatgatgac agatttactg tttcagtga 180
tgctagctgt catgatttgag tcctgtaaaaa gattatatta agctaaaact aactgtaaaa 240
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cttccctctt tccctctctc ctatctacca ggtgccttgc gctaactttt cattcagagt 360
gtttctgtc ccttacaaag ctgacagagt tgtcaagagg tttcaccac tcaaccac 420
ttacttgaca cacagttact tgcattacaa agcactgcat gaggagctt tgtaataaaa 480
gggtgactc aaacacagat cctccctcc agggtcacgt ctgtgctgtt gaatgtgaa 540
ccaaatgact acattactaa ataaaaaaaaa aaaaaaaaaa aaaaaa 585

<210> 15
<211> 1144
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (605)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1144)
<223> n equals a,t,g, or c

<400> 15
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gctcagactt ttaatgccc ttaatctgtt tggttggcg cttcactcta ttttctggtg 180
ctgcccagcc agtgccttgc cccatggatg ttactggctt cttgagaaaaa aggagagggg 240
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agtattgaag cctcggctt ccctctggag cctgggaccc tggttacagt tgcacatctg 540
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agaangctga gctcctcatg gtgctataac cccttggac actcatccag acttctctga 660
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tcan 1144

<210> 16
<211> 1037
<212> DNA
<213> Homo sapiens

<400> 16

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ttgttcagtg	gagcacatgt	ggtcctggag	aaagctgtca	cacagtggac	tcagagatgt	180
ggtctacggg	cactaatttc	ctctcagtcc	ctgcctaagc	aagattcatc	ttccctctgcc	240
tgctgtttca	ttttttctt	ctattgtctg	gtatatctta	agataaaaaac	ttgtttccaa	300
agggaaaagt	tcagaaaatgt	ttcttaagaat	aataattcaa	gttggatttc	caagtagtat	360
tcctgggcaa	ctgattaaaat	tctttgtca	ataatcaaaa	tctggaatgt	cctggattag	420
ttccaccatt	tcatcatgat	aactccctc	tctataatcc	ctaccagaaa	tgattgcttt	480
gcttaaaaac	ttttccctga	gaagacactg	gtgtgttatt	tctttatcag	cttatgaaaaa	540
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tggcggatc	atgaggtcaa	aattgagacc	tcctarcca	acatggtaaa	accctgtctc	660
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gaggctgagg	caggagaatc	acttgatcct	gggaggcaga	gggtgcagtg	agccgagaga	780
gcgcactgc	attgcagcc	ggcgacagag	cgagactcca	tctaaaaata	tatgtatatt	840
aattctacat	atcttaggatt	tttactgtgc	ctttgttgc	tttaagct	ctgggtttct	900
caagttaaac	attaaaagta	ttatggaaagt	actgtatgt	tactcagagg	aaaacaata	960
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aaaaaaaaaa	aactcga					1037

<210> 17
<211> 925
<212> DNA
<213> Homo sapiens

<400> 17

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actggaaatc	agtttgcgt	aatatcaaa	cgattctgt	agttgaagaa	aaggagggtc	120
cagccttgc	aagaggagt	tgcccttcc	tggaaatccc	ctggacacac	cctccttagca	180
tcctctagga	aagatgcggc	agctcaaagg	gaagcccaag	aaggagacct	ccaaggacaa	240
gaaggagcgg	aagcaagcca	tgcaggaggc	ccggcagcag	atcactacag	tggtactgcc	300
cacgctggcc	gtggcgtgtc	tcttgatcgt	ggtgtttgt	tacgtggcca	cgcccccac	360
catcaccgag	tgagccccgc	agccggccgc	ggaccccccac	ggcagggaga	ggaggcgcgg	420
gagggggacg	caaacaaaaa	atggcttca	tattcagaga	tgttcatgtt	gctgagctgt	480
aagcaggagc	accctgtctt	ctctggtctt	tgacttgatt	aaagtatctc	cgcttcttg	540
ggagggaata	ggggatgttt	tatcagtgaa	tgtgccatac	accttatgtt	ccacttcatg	600
tgccttcag	acttcaaarc	gcgcgcgcac	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	660
gtgccttc	ttctctctta	aaaatcgata	atgtatcaca	cctgaagagg	gatgaaacct	720
ctgggtcagg	aaacagctgg	aatccacact	cacccatcc	ccattgtttg	gatcatgcct	780
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<210> 18
<211> 1197
<212> DNA
<213> Homo sapiens

<220>
<221> SITE

<222> (25)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (36)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (92)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (1192)
<223> n equals a,t,g, or c

<400> 18		
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ctgcacaacg	tggtcctgct ctccaccaac taccttggga caaggcgctg aatgaaccat	180
ggagcggatg	gcattgtct gcagtcgtat agtatagcag tgcaggaaca aacagcactt	240
gccagcaaag	tctgtgtcta ctgttaagtg tggggaggc agagagagga gcaggggcca	300
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gaaacaaaacc	ctcttgctag gggtgtccg tggaggtgt catcctgtcc ccctcataat	420
tactaatagc	tggacttggc agcagcctct actgggcttt tactgtatg tgttcagttc	480
atgtcctagg	aagttagctt ttgcccagg tggaaatcct tatttggctt aggactgatc	540
cacttccatg	ttacttacat ctgtggttt ttgtgttgc tgtagaaaa ttgtggctg	600
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tgtttctage	tttcaactctc cattgtctt tcttggctgt attacagccc tctgtggatc	900
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tctctggcc	atggatcaca cctgttaaggactaattact gcccagcctg gggagatcag	1020
gagaggtctg	catagtttagt aagttgggtt tagctttgt gtgtgcata gtaactttaga	1080
gttctgtaat	aacttattgt aaatgcata gacactgttt taaaacccaa gtaaagactg	1140
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<210> 19
<211> 1106
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (318)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (509)
<223> n equals a,t,g, or c

<220>
<221> SITE

<222> (523)
<223> n equals a,t,g, or c

<400> 19

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ggcagacccg	gtttgctgat	cgccccagg	atcaggaggt	aagcaccata	gaggagctgg	120
gttagagacg	agagactaa	ccgttctct	gctgaaaaag	acaactgagg	aaaggccagc	180
catgctgtgc	acacctctga	gaaccta	ctgcaa	acat	ggacatcage	240
tggttcatt	tctctttat	tcactttagc	catgtcctct	ggtgtctctg	agctgggttt	300
ccttaaagct	tcggcttncc	tttggggttt	gtctatcago	ctat	ttgtaa ggctgacttt	360
tatgccatm	gcaaatacaa	gcattttta	agttaacaga	tattatgaag	aaaaatgcaa	420
gtttttcatt	tataaggcaa	cataacttca	gagaaaaaaac	tgagtcaatc	atataaaatg	480
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aactctacat	gtataagttag	agtttctcca	gcgc	tttacca	acatataggaa aaaaacatta	780
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tcaagcttcc	ctaaaattca	caatcgtta	tttcagctc	at	aaacatct tttctgttc	900
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gtcaaacatc	tttttatgt	ttattggata	tttgagcaaa	ttgctcatc	acattttg	1020
cacactttc	aaatagactg	ttgtttctt	attgatacat	ggttctccat	gtattccaaa	1080
agcaaaaaaaaa	aaaaaaaaaa	actcga				1106

<210> 20
<211> 932
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (458)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (465)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (494)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (501)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (515)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (582)

<223> n equals a,t,g, or c

<400> 20

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ctggggcatg	gggtttggca	gaacattctg	tgaaaaatgg	atacatatat	gtttttttc	180
gtgacactt	tttlyttttg	cttttggaga	tttttcaatt	tggctccagg	acctgtatga	240
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tgcataaaat	gacttccct	cctgtggaaa	cagtgtccgt	ctctgaatgg	gagctttaaa	420
ggagtaggca	caaattgtaa	gatgtatgtat	cttgagggnct	gggggncttag	agatattctg	480
ctgcctccca	gagnctttgt	ngcagacggg	tctgnccagg	gtggggaaaag	ggaagcctcc	540
gttcttttg	gtaaagctagc	cataaaagaca	ggtaagggag	tnctattttc	aagaaaagctg	600
gatctgttgc	gtactcttgc	tgccccataat	cgctgtggac	agctcccagc	agcacaaaaga	660
gatgaagggc	aaaggcagga	tgcagcaggc	aaagtttaaca	ttgttatttgc	gagtagcatt	720
gagataaaa	aagggtatgaa	atccacgggt	aggaccatca	tggggggggaa	atagtttatt	780
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gtcatagaaa	cctgttttgt	gaaacctcag	atttctaaag	aaaaccagaa	gcaagacatt	900
ccttggttta	aaaaaaaaaa	aaaagggcgg	cc			932

<210> 21

<211> 1032

<212> DNA

<213> Homo sapiens

<400> 21

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atggatgtgt	acatctgtaa	tgattgtaaa	cgggcacaag	agggcagcag	tgaggaattt	180
tactgtatct	gcagaacacc	ttatgtatgt	tccacaatttt	atattggctg	tgatcggtgt	240
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gaggatgtct	gtccacagtg	ccagtc当地	gaggatgcc	tgacagtgct	cacgccacta	360
acagagaagg	attatgaggg	gttgaagagg	gtgctccgtt	ccttacaggc	ccataagatg	420
gcctggcctt	tccttgaacc	agttagaccct	aatgtatgcac	cagattatta	tgggtttatt	480
aaggAACCTA	tggaccttgc	caccatggaa	gaaagaggtac	aaagacgata	ttatggaaaag	540
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agtactccc	cattttacca	gtgtc当地	gttctcgat	catttttgt	acagaaattt	660
aaaggcttca	aagctagcag	gtctcataac	aacaaactgc	agtctacagc	ttctttaaaat	720
tcagcgtgtt	aacctaacat	aaaacacagc	aagaatctgg	ttgtctgaac	tattttaaaat	780
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gcaaaagtcaa	cgacaccatt	atcttgc当地	gatcagatgg	ttttactatt	gtggcagaag	960
cgagaaaact	ttgtttatgg	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	1020
aaaagggcgg	cc					1032

<210> 22

<211> 487

<212> DNA

<213> Homo sapiens

<400> 22

acgttagtgg gaaaacgtgg	60
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cattttagta atgtgttaaa	240
tgtgatttt ttatTTTtta	300
ggtgtggta ggtgtgttga	360
agatgactta agaagcatcc	420
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ggcgccc	487

<210> 23

<211> 1460

<212> DNA

<213> Homo sapiens

<400> 23

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gtcgcgcccc cttaagagc	120
caggTTTca aaacaaaaat	180
aactacttat gcagaaccag	240
gaccctctct taataaggac	300
agaaggcagc tttgcagcat	360
ctgcatttgg gaacttattc	420
tttgcgtatgg aaaagtact	480
catgaactgt gacttaaga	540
aggaatgtgt aagtgaaagc	600
gtatcgcca aggaatttat	660
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actgaatata tcatgtccac	780
gaaacaaggc tgctttaaa	840
ctgtttatag gattgctata	900
aaatatttct tctggactta	960
aataaattac taaccagtct	1020
actagatgca attaaaaata	1080
tttagtgtta ccacataaat	1140
tgaaaacttt ttggctgggc	1200
aaggcgggca gatcacttga	1260
cctgtctcta ctaaaagtat	1320
agctactcag gaggctgagg	1380
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aaaaaaaaaa aaaaactcga	1460

<210> 24

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 24

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gccccatgtt gctcaagtgg	300
cctggccgc tcccggcgc	360
ggaccccgac cgaggcttca	420
tgggTTTctg ttcttgacaa	480
gcggcatgct catcagcg	
ctgggcattt gggtccctgg	

atgtggctcc aactgggcgc aggaaccgct aaacgagaca gacactggcg actcagagcc	540
ccggatgtgt gggttcctt ctctgcagat catggggccc ttgattgtgc ttgtggatt	600
gtgtttcttc gtggttgccc atgttaagaa gagaacacccg ctgaatgtgc gccaggatgc	660
ctctgagaga gaagarggac agatccagat tatggagcc tgcaggatca ctgtagcttc	720
tgcggcgcgt gagagtccgt gaactaacag tctgcttccg aatgaaaacc ccccttcata	780
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tgaatctata tataccattt ctgggacgaa ttcatgttccg aagggctcac acactccaca	900
tctccatct gaattgcctc ctagatatga agaaaaagaa aatgctgcag ctacattctt	960
gcctctatct tctgagccct ccccacccgtaa aactatggac tctagttcag ttttatatgc	1020
aatggatcac tatttttattt aattttttt aaataaaaaaa tacaatagca aaaaaaaaaaa	1080
aaaaaaaaatga ccctcgaa	1098

<210> 25

<211> 1015

<212> DNA

<213> Homo sapiens

<400> 25

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gacctgtttc cttaaaaaat ccatttttag acaacactata gcattaagat tgaatccaa	360
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gccatgaaag tggaaagtgaa accttttaa ttaattttct ttggcagttt gaaatggccc	480
atgttttagc tggtagcaat gtaagtttac atatgagccc aactaagctg gttcattatt	540
ctcttcagtt gtttgaagt tggcagccat catcacaaca gcagctggat acaagataac	600
ctagccagtg ttggcacatg ttgaggcata tggaaatttt ttaatcatg caacccctgc	660
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tatgacttaa attattctat tcagattttt taatccaaattt gaacattaaac tgagtaattt	780
gatgttttta tctaaatgga taagatgatt ttttgaagta taaaatggga tttttagggaa	840
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gtgtttggct ggggtgcagtg gctgacaccc ttaatccaa tactttggga ggctgaggta	960
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<210> 26

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 26

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gagaagacga cagaagggtt cggctgcgag aagacgacag aagggtacgg ctgcgagaag	120
acgacagaag ggtacggctg cgagaagacg acagaagggt acggctgcga gaagacgaca	180
gaagggtacg gctctttctc cgctccgcgg ccctctctcg tccctccctc aaggcgcggaa	240
rgcggaaacct ctccacctt tccgagcggg gtmacggccc ggcyygcgttta acctggtttc	300
cgagagtgcg gggcggtcgg cgggtcaggg cagccccgggg cctgacgcca tgcggccaa	360
cctgcgcacc ggcgtcattt tcggcggctt catctccctg atcggcggcc ccttctatcc	420
catctacttc cggcccttaa tgagattgga ggagtacaag aaggaacaag ctataaatcg	480
ggcttggaaatt gttcaagagg atgtgcagcc accagggtt aatgtgtgtt ctgatccatt	540
tggcaggaaa tgagagggtt gtcatcgat ctgatataa aaggagattt ctcatgtt	600
tcgattctgc atggggtaca gccagtccacc tcaccagaga atgacggctg gagaagaaaa	660
ctctgttaata ccataaataa gagtgcgtt aataaaaagac tgcacaag gattaatatt	720
tcccttcata agtataaaaaa gaactctgga acaaattata ccattagaa gggtttcatg	780
attcagttga ttttccaaaaa atgaagctat ctcaccccagc tgggtttgga ggagcaatct	840

gcttattatt	ctgtcgtaac	cacttactca	agcgagctgt	gatataaata	caaggcaacca	900
gtgggctcg	gaaggctccgg	gtctttctg	ccatcttcca	gataagagat	ttcagtaaaa	960
aactgccat	ctgagctgcc	ttatagagct	cttcgaaaaat	gttcgagttt	ataaaagctct	1020
ttgaggacaa	ggtacttcgt	gcacctcatg	ctgaagattt	caccatgttg	aaaaataaaat	1080
atgaagcaag	tcaaactaga	tgcatacact	tgtgttagaaa	tcaataatca	attaatagaa	1140
gtaaaaaaaa	agacattaaa	atgattttatt	tctaaaaaaaa	aaaaaaaaaa	aactcga	1197

<210> 27
<211> 1002
<212> DNA
<213> *Homo sapiens*

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<220>
<221> SITE
<222> (19)
<223> n equals a,t,q, or c
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<220>
<221> SITE
<222> (29)
<223> n equals a,t,g, or c
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<220>
<221> SITE
<222> (948)
<223> n equals a.t.g. or c
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<220>
<221> SITE
<222> (955)
<223> n equals a,t,q, or c
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<220>
<221> SITE
<222> (969)
<223> n equals a.t.q. or c
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<220>
<221> SITE
<222> (973)
<223> n equals a.t.g. or c
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<220>
<221> SITE
<222> (990)
<223> n equals a,t,q, or c
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<400> 27

tgc	cccttccc	tgc	ccctgtnt	ccg	ccgttnt	tcc	ccccaccc	ccg	ccccata	gac	ccaagttc	60
gt	gcagtgc	c	agatggga	g	ctccagaaa	c	gcaaggagg	t	ggtgacac	c	gtgtccctg	120
cac	cgagatcg	a	cgtcatcaa	c	tctcgacc	c	agggcttcc	t	ggcgcttct	t	tcaggtgac	180
ac	aggggaga	t	caagtca	g	atccgttag	c	agatcaatg	ccaa	aggtggc	t	gatggcgc	240
gagg	aggggca	agg	ggagat	cat	ccctgga	gt	gctgttca	tgc	acgaggt	cc	acatgctg	300
gac	atcgaga	g	tttcctt	c	tcaaccgg	gc	ccctggaga	gt	gacatggc	gc	ctgtccctg	360
at	catggca	cc	aacgtgg	at	cacgcga	at	ccggggca	cc	agcttacca	ga	gcccctcac	420
gg	catccccca	ta	gacctgt	gg	accggctg	ctt	atcgct	cc	accaccccc	ct	acagcgag	480
aa	agacacga	agc	agatccct	ccg	catccgg	tg	cgaggaag	a	agatgtgga	ga	tgagtgtgag	540

gacgcctaca	cggtgctgac	ccgcacatcgaa	ctggagacgt	cactgcgcta	cgccatccag	600
ctcatcacag	ctgccagctt	ggtgtgccc	aaacgcagg	gtacagaagt	gcaggtggat	660
gacatcaagc	gggtctactc	actcttcctg	gacgagttcc	gctccacgca	gtacatgaag	720
gagtaaccagg	acgccttcct	cttcaacgaa	ctcaaaggcg	agaccatgga	cacccctgaa	780
gttggatgtc	atcccccgac	cccacccctgt	tttccaccag	agttctgaca	ctgtactct	840
gtataaaaatg	gttggaaagc	tgcaaaaaaaaaa	aaaaaaaaaa	aaactcgagg	ggggccgggt	900
acccaattcg	ccctatagtg	agtcgttatta	caattcatgg	ccgtcgtnntt	acaangtcgt	960
gactgggnna	aancctggcg	ttacccaatn	aatcgcttgc	ag		1002

<210> 28

<211> 1327

<212> DNA

<213> Homo sapiens

<400> 28

ggcacgagga	aagtccctgc	tctggtgacc	tgttaagttgc	agaggaggggt	ggagttagag	60
tgtcatgtat	tgggatagtc	agggatccct	gcctttggcc	tttcttcctc	ttcttcttcc	120
tcttccatag	ttggatcatg	tatattwac	ttctaaagga	gagaatgtca	aaaagttctg	180
tatTTTTTta	tattctatat	attaggttag	tcaatcttaa	ttggtctcaa	gaggaagaac	240
tgtctgtcat	ttcggtaagt	aggatactgt	gaggaagacc	aaaaagagat	atggatgctt	300
cctcgctcag	gaggcctgag	cttggcctt	ttcctctctg	cttggattct	ggaccaccac	360
ctgggaccaa	cttcagctc	tggAACCTTC	ataaaagcagg	tcagcgtggc	ctgattgtcc	420
caggacctga	agggagcaag	gatggcctca	gggcctgggt	aagtctgcta	ctctgtcctt	480
actgctgaac	atcctgctt	tatcaggaaa	ctcagaagca	gtttgcctt	tcaaatcaat	540
ctcaatgggc	catgtccaca	taactgatca	ccatggctg	cctctccat	tatctattat	600
cactgaaaact	tagtagcctg	ctctttttt	ttttttttt	agagctattt	cgtatcttcc	660
ctgtttggga	tccttgcatt	tggtttgggt	tttcccttcc	ttgtgacaat	tataatccag	720
atgcctcttc	tttctgtttt	aattacggta	gtgcattgcc	ttagtgccct	gcctgtgcct	780
ctgggtggat	tacatatgat	agtaaagccc	acctgtttgg	atgggatgt	aggaagttgg	840
tgttagaccag	ctgtggagct	gaaggcacag	tctgccccac	ccccacctcc	ccactgtgg	900
tagtcagagg	cattctgctc	caagctctgc	tttcccttcc	tctgaaacaa	tgccattctt	960
gcttctatttgc	ctacacatct	ccttctggct	caggtgaaat	ccatgcctt	ctgtttatag	1020
acctaaagtt	caggtactta	ttattggcca	ttgatcttga	atttgcctc	tcctagtgt	1080
gcagtcac	ttcaaagcca	ttttctgagg	aggatggttt	aggctctggca	attgtccttgc	1140
aaaaatccca	cccatgttgt	accacccctgg	ttagtcatat	gccactcatc	agcttggaa	1200
tgatggctgc	caactcccaa	tctcccagga	aggcaggggg	cagaatctt	tttctacttgc	1260
gcctgttacc	tccattaaaaa	aaccattctc	ttacagtttta	aaaaaaaaaa	aaaaaaaaaa	1320
ggcgccc						1327

<210> 29

<211> 668

<212> DNA

<213> Homo sapiens

<400> 29

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ttcggttctt	cagttttctg	agaagagttt	ggatatgtgg	gaagggggcat	gggagctcgg	120
cagccctccgc	ctgccaggaa	ggcagtttcg	cctctgcagg	aaagagcaga	gcccgtggaa	180
agccctgggt	gagggtggcg	cagcggccca	gcacgcattgg	tattgccagg	cacggggggc	240
ctgcgtgtag	tctctgtctc	ctgcatttca	ccttctttgt	tgactttct	tctctgtttt	300
cccccatctg	tttgccagag	gggtgggact	ggcaacagaaa	cagccgtggc	tgctttatct	360
ctccctctcca	cggtgtactc	aggcctgagt	ggtgactcac	gggagccctgg	ccacccctcgca	420
gctgttcgccc	ccctcaacct	ttgaactgg	actgctggct	cacacaggg	tttgcacaac	480
tgcagctgaa	tctcatggaa	aagctggatt	cctctgcctt	acgcagaaac	acccggggctc	540
catctgcccag	gtgcttgcca	ctggctctgg	cagaatggc	ggctgctgaa	agtgcaccc	600
caaattccctg	gtggcacttc	agcgcacag	gctctccaaat	aaaaacccctt	tacacacaaaa	660

aaaaaaaaa

668

<210> 30
<211> 1243
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (327)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (335)
<223> n equals a,t,g, or c

<400> 30

ggtcgaccca	cgcgtccgat	tttataaaaa	gtacagttt	acattccatt	taccttgtta	60
cttttgact	acaagtctt	gttccctt	ccagtccctc	ttcccagttc	ttgaccaaat	120
acacctaaaa	aaggaatgtc	acatttatgg	aactgtgtga	tctttctttt	aatctggttt	180
aacattaaac	tatgggtttt	ttgttgtt	tctttgtat	aagttccacc	tgctatacac	240
tgttagcgca	aagtattttt	ttggAACACT	tttgttattag	ttatggaaat	aaatTTTACA	300
cattggatta	aaatgttagag	aaACATNCAT	tgagnataCT	cagcaAGTC	TGCTGGACTA	360
gaagctgtta	cttctgtta	aatgactcta	matmtcttt	ctwyaaacca	ctatctactg	420
tytcatagtt	taactccaa	agcaggTTTT	gtttgtttc	cctaagctct	tagataaaatc	480
ctcagggata	tctcagtgc	tgacatattt	tattataatt	gcttgtttgt	ctatttctcc	540
cactagaaac	tatggatgt	tggtgagaat	ttcacagcag	gaaagatgg	gaaggTTAAAG	600
gatctgaaca	ggagtttaggt	aggaaagtat	tacatgctat	gatgttagctg	tatataaccac	660
caaaaattct	accttagaaat	ggtttaggtc	actgaatttc	ataatTTTAC	aattatttca	720
tattccctta	cataagaatt	tgtatgttgc	aaggcttaag	aagctttaat	ttatcagttc	780
ctattagcgt	atcgtcctct	ttttgtgtca	agaaaaagaaaa	ctcggctggg	TGCGGTGGCT	840
cacgcttgta	atcccagcac	tttgggtggg	aggccgaggc	agcgaatgg	ttgcctgagg	900
tcaggagttt	gagaccagcc	tggctgacat	ggtggggaccc	tgtctctgct	aaaaataaaaa	960
aagtttaggt	ggtgtgggt	tgtgtgcctg	tggtcccagc	tactggggag	gctgaggcag	1020
gagactctct	tgggcctggg	aggcagaggt	tgcagtggc	cgaggtcatg	cccgcgtcac	1080
tccagcctgg	gcaacagagc	gagactccgt	ctcaaaaaaaa	atataataaa	cctcattctt	1140
ttatTTTTAA	ggtaatattt	tttactggta	aaaatttgata	aaaataagcc	aaagacaacg	1200
attcaatctt	aatctcatag	aaaaaaaaaa	aaaaaggggcg	gcc		1243

<210> 31
<211> 1053
<212> DNA
<213> Homo sapiens

<400> 31

attacggaat	acagtagaca	ccatgttaacc	ccagtcttaa	tatTTAAAGA	atgttaatgt	60
tgtcacattt	ctatctttt	tttttacatg	agaagtcaaa	cattacatta	taagtagagc	120
taaaatccaa	cctctccatc	ccctttccag	agctaatgag	gagcttGatt	gtAAATTGTT	180
tgtatATCAG	ctctgtgc	ttwAAAATAT	attcatccct	tatctgtatt	ggtaacaatg	240
cttattaaatg	tttatctgtt	tattttttt	gttttcatc	agcttttgc	ttcctcattt	300
ctgagattag	gtcatgttga	tacatacgt	aattaaattt	ctagatagta	ttcgtcaaa	360
ttcccttact	acttgtgtgt	acttaatctt	gttttagtatt	tttttattgt	ttcattcaac	420
aatatgttct	gagattgagt	catgttgata	catatagaca	atTTTATTtT	tattactata	480
gaaagatctg	ttaaatgaat	atagtctatt	taccaacttc	aacagaattt	taatataatt	540
agTTTTAGC	tgttagagac	tctactccag	tgaacctgtt	tcctcattca	gargaatgt	600

tagtttatgt tctcagaaac agaatttcat ggctggcat aatggctcat gtcttggga	660
rgccaaaggc caggarttg agggcaacct ggacaccaca gcaagamccc atcttacaa	720
aattttttat taaaaattaa ccagggccgg gtgcagtggc tcatgcctgc actttggag	780
gctgaggtgg gcggatcacc tgaggtcagg agttttagac cagcctgacc aacatggaga	840
gaccggctct ctactaaaaaa tacaaaattt gccgcgtgtg gtggtgcatt cctgtaatcc	900
cagctgctca ggaggcttag gcaggagaat tgcttgaacc caggagacgg aggttgcaaa	960
gagccgagat tggccattt cactccagcc tggcaagaa gagcgaaact cggtctcaaa	1020
aaaaaaaaaaa aaaaaaaaaa aaaaagggcg gcc	1053

<210> 32
<211> 1014
<212> DNA
<213> Homo sapiens

<400> 32	
ggtcgaccca cgcgtccgaa acttaaaaaa atgtggccag gcatacgtagc tcatgcctgt	60
aatccttagca atttgggagg ccgaggccgg agatccctt gaatccagga gttcgagacc	120
agcttggca acaaacttag accctcatct ccatatatta aaaaaataaa aaataaataa	180
ttgtttttttt aaaccacaca aaaaatgtat aaacatgtat cccctgtact gcaaaatctt	240
gctctcatcc ctattccccc tgctctttc caaccatacc tatgttagcta accacattta	300
ttcattctgg ctcattcttt atatgttttct tcttgc当地 ataagcaaac tgtatataatt	360
taatatttctt acttacagaa aatgttagtat atatactcct ttgcacccctt tattttgtt	420
tgtttactta agaatatatt ccagaaatca ttctacatta gttcataggc atcttttga	480
ctattattat ggccagtttc taaaatggct gcatagtact ctgttgtatg gttgatctt	540
gcttttagtcg accttctgtt aatggaaatt attatggaga ttagcttta gagtaaattc	600
ctagaagaat gattgctgtt caaagagtaa atgcataatgt agtttattttt gatgtgtca	660
aatttccttc catatgagca gcacacaatc actttaaaaa ggcactttt tggccggcgc	720
tggtgctcac gcctgtatcc ccagcacttt gggaggccag ggcaggagga tcatgaggc	780
aggagatgga gactattctg gctaaccagg taaaaccctg tctctactaa aaaataaaaa	840
aaatttagccg ggcgtgttgg cgcatgcctg tagtcccagc tactcaggag gctgaggcag	900
gagaattgct tgaacctggg aggccagaggt tgcaagtgc tgagatcgca ccactacgcg	960
ccagcctggg caatagagcg agattcgtct caaaaaaaaaa aaaaagggc ggcc	1014

<210> 33
<211> 1373
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (1373)
<223> n equals a,t,g, or c

<400> 33	
gaattcggca cgaggacgct tcggccgtaa cgatgatcg agacatccctg ctgttcggga	60
cgttgctgtat gaatgccggg gcgggtctga actttaagct gaaaaagaag gacacgcagg	120
gctttggggaa ggagtccagg gagcccaagca caggtgacaa catccggaa ttcttgcgt	180
gcctcagata ctttcgaatc ttcatgcctt tggaaacat ttcatgtat ttctgcattga	240
ttgtgtgtt cggctcttga atcccagcga tggaaaccagg aactcacttt cccggatgc	300
cgagtctcca ttccctccatt cctgtatgact tcaagaatgt ttttgcaccaaaaacgcaca	360
accttcccag aaagtccaaat ctcgtgttgg gtggaaaatgt ttgcggcagg gtgtgcattgg	420
tttcccagcc acgtccctgt ttcaaaatgtt agtttcaattt tggtctctga attgaaatgc	480
tgtctactga aagggtttca ggagcgttta tggaaaggcgg tggatgaaaa ttgcattccc	540
catagataaa agaaaaatca ttctatcca gagatctgag cagaaggatt ggcttgcatttag	600
tttaacacag ccgtatcccccc ggacattcag tggacttgc tgagtcgtac agcctctggg	660
cccgccagg ggcctgttta acaaactgct ttccatccc aacagggtct gcttggccac	720

tcagtgcagc	tgcgattaac	cctaaaggct	ttaaggaacg	ggccacctgt	aacagagaca	780
ccagccttcc	tgtatagaca	ctaaattgtt	agcaagagtg	tttagctagt	tcctgggtaa	840
gtgtttccac	agaagacatg	tggagcagtt	gtggggatat	taagggaaac	tttcctctgc	900
cttgaccctt	ttgtttaata	aatgacttt	gggagccatt	cattgtacag	ttgcaggaat	960
gagagtgatt	ttatgatgtg	gtacattggg	accatgttct	aaaaccttg	gtttctgagt	1020
ctgcttttg	agtaggttat	tttgagggtt	aaaaaccagg	ggccttcattc	taggaaatac	1080
agcattttcc	agaagcttct	ttgaaaggga	atccctggtt	tgttgccaaa	atgaaacgcc	1140
cgggggttggc	gctgaatccc	acaactgtgt	gatttgcttg	ttgagtttt	tgttgtctgg	1200
ttttttgtt	tgttgttta	taccaataag	aatgagcctg	aatgttggtg	gttttgaaa	1260
tcctgacttg	gaggtaaacc	tggaggaagg	aaaaaaaaagta	aatatgcagg	cttttaggac	1320
tgagtagcct	tgaaaataaa	cctcatttct	aaaaaggaaa	aaaaaaaaaa	aan	1373

<210> 34
<211> 1404
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (36)
<223> n equals a,t,g, or c

<400> 34						
gtggatcccc	gggctgcagg	aattcggcaa	cggcgncgc	tccccgtcc	tcctcccccag	60
ccatggcggt	cacgttcgcg	gccttctgct	acatgctggc	gctgctgctc	actgccgcgc	120
tcatcttctt	cgccatttgg	cacattatag	catttcatgt	gctgaagact	gattacaaga	180
atccatataga	ccagtgtat	accctgaatc	cccttgtact	cccagagatc	ctcatccacg	240
ctttcttctg	tgtcatgttt	ctttgtgcag	cagagttggct	tacactgggt	ctcaatatgc	300
ccctcttggc	atatcatatt	tggaggatata	tgagtagacc	agtgtatgat	ggccaggac	360
tctatgaccc	tacaaccatc	atgaatgcag	atattcttagc	atattgtcag	aaggaaggat	420
ggtgcaaaatt	agctttttat	cttcttagat	ttttttacta	cctatatggc	atgtatctatg	480
ttttttgtgag	ctcttagaac	aacacacaga	agaattggtc	cagttaaatgt	catgaaaaaa	540
gccacccaaat	gaagggattc	tatccagcaa	gatccgttcc	aagagtagcc	tgtggaatct	600
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ttataggaac	ttgttagggct	cattttggtt	tcattgtaaac	agtagatctat	tataaaattag	900
ctgtagatat	caggtgtttc	tgatgtgt	aaaatgtata	tctgactagt	gggaaacttc	960
atgggtttcc	tcatctgtca	tgtcgatgt	tatataatgg	tacatttaca	aaaataaaaaa	1020
gcgggaattt	tcccttcgt	tgaatattat	ccctgtatat	tgcatgtatg	agagattcc	1080
catatttcca	tcaagatata	aaatataactt	gctttattc	ttaagcataa	gtaaacatga	1140
tataaaaata	tatgtgtat	tacttggaa	gaatgcattt	aaagctattt	taaatgtgtt	1200
tttattttgt	agacattact	tattaagaaa	ttgggttatta	tgcttactgt	tctaattctgg	1260
tggttaaaggt	attcttaaga	atttgcaagg	actacagatt	ttcaaaaactg	aatgagagaa	1320
aattgtataa	ccatccctgt	gttcctttag	tgcaatacaa	taaaaactctg	aaatataactc	1380
aaaaaaaaaa	aaaaaaaaact	cgta				1404

<210> 35
<211> 1093
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (2)

<223> n equals a,t,g, or c

<400> 35

<210> 36

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (72)

<223> n equals a,t,q, or c

<220>

<221> SITE

<222> (417

<223> n equals a,t,q, or c

<400> 36

aaaatgttca atcatctatg tcattttaaa atgtttaaaa cacttttag ctttctaaca	60
tattccccat gnaaataaaa aatgtacatg tcttatctgt tttactctt tggtatgtcac	120
gtttttaaac ttaattttc ttttccttta aactactgtg tggactttta tcaactactg	180
ttttatattc acctaattgt gtagtaaata ttttaagata ataacctgga gaatttgagg	240
aaagtcaaat atgtgtgaaa ctctttttc ttcccccgtt gcttttaggtt caaatttattt	300
ggctcgactt ctatgttttgc tcttattttca ggcagctctg tccagttggag tgaccggktg	360
ccagagtgcg gaggttaagag ttaaaaaaaaac ctaagcacct ccaggatggt qaaggcnq	418

<210> 37

<211> 1042

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (222)

<223> n equals a,t,q, or c

<400> 37

gaatcgac	gaggaaatat tactgaattt tcttttatta tcaaatacaa atttagcata	60
tcctatgtaa	aatgctgatt gccccttct gcatttattt tcagatcttgc ttccatatac	120
ccacaaggat	tttctatata tttctcataa acaagagagt ccacatattt actacttacc	180
ttatgagtga	acaaaaaaaaat cacgattggg ttcgcagaac tncaaaggat caccgtgtgt	240
ggctcattag	tggaaaaatctg ctgctgttg cagatataaa ggctctgatc aggtggctgt	300
ggggccctaa	tccagaatga gcacagttat ttgatcaat ggagtctaac ctatgcctcc	360
cccaaggatc	aaaatgtcct ctgggtcttgc caatttctt acagtatccc ttcttaattt	420
ataccaagct	gggactctcc ttgttatcatca tattttggaa tgaaaatgaa aacaaatgag	480
aattttcctt	ttgcgttggtaatgcatac agtgattttaa gtttgggtgc attttttca	540
gtctgttgc	ttgttcttaga atcgatgctc acagatcaat gagtcatgtc caatttcata	600
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gaataaaacat	ttttagggcgggtgtgt gtcatgcct ataataatcag cacttggga	780
ggccaaggca	gaaggattgc ttgaggcttagt gatgtggaga ccagcctgag taacatagt	840
agaccccagt	ccttacaaaa aaaaaaaaaa attaacaag gattgtgtgt catgcctgt	900
gtcttagcta	ctcgggagc tgaggaggaa agacaactttt aaccgggagttcaaggtr	960
cagtgcata	attgcaccat cgcgatccag ccttggtgac agagcaagac tctgtctcaa	1020
aaaaaaaaaa	aaaaaaaaactcg aa	1042

<210> 38

<211> 798
<212> DNA
<213> Homo sapiens

<400> 38

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gattaaaact	atttctcttgc atttttgttgc ttgactgttgc gtttttgc aatcttgcgc	180
tcatacagct	tcatctgggt ggtcggtgg ggactggact tgagtaggt ggctgggtct	240
ccttccatgt	agtcgctcgt cttaggccttgc ttcacagcat ggtgtcttgc ggacaggagt	300
arcagctgt	aggcccttgg ggctgtgggt tagaaattat accacgttgc ttctctgttgc	360
caaagcaagt	cacaagtccatc gttcttatttca aagttttgg gtaaataggc tataatcttgc	420
gattggaggt	gctgttagaga ttctctggcc gtatatttgc ttcaacatca gtatagttgc	480
atgaatgctg	tgggttagat gagcaaaaggg tgctatagaa cagaggatgg aaacctaaatt	540
cagcttgagg	gaagggtcaa ggaaggcttc ttggagttgg taatgttgc cgtaagccct	600
ttaaataaaaa	gtattatgttgc atgggtgtgt tatagaaaac ataaaggat ggcggggcgt	660
gatggctcac	acctgtatcc ccagcacttgc gggaggccaa agtggggagga ttgggttgc	720
tcaggagtttgc	agaccagccttgc aggcaatataa gtgagagccttgc atctctttat atattaaaaa	780
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<210> 39

<211> 1030
<212> DNA
<213> Homo sapiens

<220>

<221> SITE
<222> (431)
<223> n equals a,t,g, or c

<400> 39

gcactgggg	caactgccttc ttctctcatgc ccaaccttccctt ccatttacttgc ttccatcttgc	60
gaagatatcc	tagtgtgtgtt agggtaagtt tggtgtgtt ggccatgttgc cacagatttt	120
atctgcttgc	ctgttttgc ttttatttgc caaataatgc ctctgttgc ttttgcata	180

ttccttcctg ttgtgggatt ccaccagttc tacactctac agcagaactc tgccattcat	240
agtcaaggac tgcagattcc ctcttcaatc tcacatcttgc gtttcttaag gatttcctgg	300
ttgtcaattt tgagttctcc ttttttttca aaacttaact atccatgtt catgtgcacc	360
tatttggta ttatgcacaa catttctatt attttaggg agtttagcatg ggaagggaaag	420
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ctgtatgtca tcagcaatgt gttgaactgg attcagttga actggaaaag tatgggtgga	660
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gcaaattcaa acatcaaagt attatatata gtaaatgaaa tttactaaga tattatcaag	840
tattaacaag ttttttagac aattgttagag tttggggga aaattgttgg ttacaatagg	900
gaaataaaac gttacttttc agtctgtatt ggatttagttt agaccagaga aaaagacatg	960
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ctagtctcgaa	1030

<210> 40
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (37)
<223> Xaa equals stop translation

<400> 40
Met Ser Leu Pro Ala Ser Phe Phe Phe Lys Ile Ala Leu Val Phe Leu
1 5 10 15

His Val Phe Ser Val Asn Phe Arg Ile Ser Leu Ser Val Ser Thr Ser
20 25 30

Pro Leu Gly Phe Xaa
35

<210> 41
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (33)
<223> Xaa equals stop translation

<400> 41
Met Ser His Phe Thr Phe Pro Leu Phe Leu Trp Gly Gln Leu Leu Phe
1 5 10 15

Asn Thr Pro Cys Gly Leu Pro Ser Trp Arg Leu Cys His His Tyr Gln
20 25 30

Xaa

<210> 42

<211> 92

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (35)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (36)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (92)

<223> Xaa equals stop translation

<400> 42

Met Gly Leu Pro Ser Ser Ile Pro Arg Leu Val Leu Leu Glu Leu Ile
1 5 10 15

Met Ala Gln Cys Ser Ser Leu Trp Lys Cys Pro Arg Gln Pro Arg His
20 25 30

Ser Leu Xaa Xaa Leu Ser Asn Thr Thr Leu Gln Ala Ala Val Thr Asn
35 40 45

His Gln Ser Ser Ala Glu Ala Ser Ser Leu Cys His Pro Cys Asn Asp
50 55 60

Ser Leu Arg Pro Cys Pro Lys His Ser Gly Leu Ser Asn Thr Gln Asn
65 70 75 80

Cys Asn Val Ile Phe Cys Ser Asn Leu Asn Phe Xaa
85 90

<210> 43

<211> 33

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (33)

<223> Xaa equals stop translation

<400> 43

Met Val Gln Gly Ser Gly Gly Thr Cys Leu Met Met Thr Asp Leu Leu
1 5 10 15

Phe Ala Val Met Leu Ala Val Met Ile Glu Ser Cys Lys Arg Leu Tyr
20 25 30

Xaa

<210> 44
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (53)
<223> Xaa equals stop translation

<400> 44
Met Asn Phe Ile Trp Ile Leu Ser Arg Leu Ile Leu Glu Ala Ser Cys
1 5 10 15

Tyr Asp Phe Leu Phe Leu Gly Ser Thr Thr Leu Tyr Ser Gln
20 25 30

Leu Thr Ala Ala Phe Arg Pro Gly Leu Gln Leu Leu Ser Ser Arg Lys
35 40 45

Cys Val Pro Val Xaa
50

<210> 45
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (26)
<223> Xaa equals stop translation

<400> 45
Met Phe Leu Arg Ile Ile Ile Gln Val Gly Phe Pro Ser Ser Ile Pro
1 5 10 15

Gly Gln Leu Ile Lys Phe Phe Cys Gln Xaa
20 25

<210> 46
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (38)
<223> Xaa equals stop translation

<400> 46
Met Gln Glu Ala Arg Gln Gln Ile Thr Thr Val Val Leu Pro Thr Leu

1 5 10 15
Ala Val Val Val Leu Leu Ile Val Val Phe Val Tyr Val Ala Thr Arg
20 25 30

Pro Thr Ile Thr Glu Xaa
35

<210> 47
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (58)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (71)
<223> Xaa equals stop translation

<400> 47
Met Cys Ser Val His Val Leu Gly Ser Gln Leu Leu Pro Gln Val Gly
1 5 10 15

Ile Leu Ile Trp Leu Arg Thr Asp Pro Leu Pro Cys Tyr Leu His Leu
20 25 30

Trp Val Phe Val Val Ala Val Arg Lys Phe Val Ala Gly Glu Asn Ser
35 40 45

Thr Pro Leu Ala Gly Ala Leu Val Ser Xaa His Val Leu Gly Cys Phe
50 55 60

Pro Pro Ser Phe Leu Ile Xaa
65 70

<210> 48
<211> 60
<212> PRT
<213> Homo sapiens

<400> 48
Met Leu Leu Leu Trp Lys Ser Leu Ile Ala Asn Asn Val Lys His Leu
1 5 10 15

Phe Tyr Val Tyr Trp Ile Phe Glu Gln Ile Ala His Ser His Leu Leu
20 25 30

His Thr Phe Gln Ile Asp Cys Cys Phe Leu Ile Asp Thr Trp Phe Ser
35 40 45

Met Tyr Ser Lys Ser Lys Lys Lys Lys Lys Leu
50 55 60

<210> 49
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (14)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (40)
<223> Xaa equals stop translation

<400> 49
Met Glu Tyr Ile Tyr Val Phe Phe Arg Asp Thr Phe Phe Xaa Leu Leu
1 5 10 15

Leu Glu Ile Phe Gln Phe Gly Ser Arg Thr Cys Met Met Phe Ser Ser
20 25 30

Phe Ala Glu Met Leu Lys Ile Xaa
35 40

<210> 50
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (104)
<223> Xaa equals stop translation

<400> 50
Met Asn Leu Ser Ser Ile Leu Ala Val Ile Phe Val Leu Thr Gly Ile
1 5 10 15

Met Glu Asn Val Leu Ala Ser Gln Lys Arg Arg Leu Arg Lys Trp Met
20 25 30

Cys Thr Ser Val Met Ile Val Asn Gly His Lys Arg Ala Ala Val Arg
35 40 45

Asn Cys Thr Val Ser Ala Glu His Leu Met Met Ser His Asn Phe Ile
50 55 60

Leu Ala Val Ile Gly Val Arg Ile Gly Thr Met Gly Ala Ala Leu Ala
65 70 75 80

Ser Cys Lys Val Arg Gln Ser Ser Leu Met Ser Met Ser Val His Ser
85 90 95

Ala Ser Gln Gln Arg Met Pro Xaa

100

<210> 51
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (23)
<223> Xaa equals stop translation

<400> 51
Met Ile Phe Leu Phe Leu Phe Cys Thr Leu Leu Asp Asp Cys Glu Ala
1 5 10 15

Met Ser Ile Gly Leu Gly Xaa
20

<210> 52
<211> 85
<212> PRT
<213> Homo sapiens

<400> 52
Met Gln Asn Gln Ser Ser Thr Asn His Pro Gly Ala Ser Ile Ala Leu
1 5 10 15

Ser Arg Pro Ser Leu Asn Lys Asp Phe Arg Asp His Ala Glu Gln Gln
20 25 30

His Ile Ala Ala Gln Gln Lys Ala Ala Leu Gln His Ala His Ala His
35 40 45

Ser Ser Gly Tyr Phe Ile Thr Gln Asp Ser Ala Phe Gly Asn Leu Phe
50 55 60

Phe Leu Phe Tyr Leu Ala Leu Thr Gln Asn Glu Glu Asn Ile Cys Asp
65 70 75 80

Gly Lys Val Thr Leu
85

<210> 53
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (74)
<223> Xaa equals stop translation

<400> 53
Met Ser Pro Ala Ala Ala Glu Pro Asp Gly Asp Gln Gln Asp Arg

1	5	10	15
His Val Ser Lys Leu Ile Phe Cys Phe Phe Val Phe Gly Ala Val Leu			
20	25	30	
Leu Cys Val Gly Val Leu Leu Ser Ile Phe Gly Phe Gln Ala Cys Gln			
35	40	45	
Tyr Lys Pro Leu Pro Asp Cys Pro Met Val Leu Lys Trp Arg Gly Cys			
50	55	60	
Met Cys Arg Gly Trp Ala Trp Gly Leu Xaa			

<210> 54
<211> 36
<212> PRT
<213> *Homo sapiens*

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<220>
<221> SITE
<222> (36)
<223> Xaa equals stop translation
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<400> 54
Met Phe Gly Ala Phe Phe Phe Cys Leu Leu Phe Lys Ser Phe Leu Asn
1 5 10 15

Gly Gly Pro Phe His Leu His Leu Ser Phe Pro Leu Lys Ser Leu Lys
 20 25 30

Pro Phe Leu Xaa
35

<210> 55
<211> 68
<212> PRT
<213> *Homo sapiens*

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<220>
<221> SITE
<222> (68)
<223> Xaa equals stop translation
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<400> 55
Met Ser Arg Asn Leu Arg Thr Ala Leu Ile Phe Gly Gly Phe Ile Ser
1 5 10 15

Leu Ile Gly Ala Ala Phe Tyr Pro Ile Tyr Phe Arg Pro Leu Met Arg
20 25 30

Leu Glu Glu Tyr Lys Lys Glu Gln Ala Ile Asn Arg Ala Gly Ile Val
35 . 40 45

Gln Glu Asp Val Gln Pro Pro Gly Leu Lys Val Trp Ser Asp Pro Phe
50 55 60

Gly Arg Lys Xaa
65

<210> 56
<211> 161
<212> PRT
<213> Homo sapiens

<400> 56
Met Leu Asp Ile Glu Ser Phe Ser Phe Leu Asn Arg Ala Leu Glu Ser
1 5 10 15

Asp Met Ala Pro Val Leu Ile Met Ala Thr Asn Arg Gly Ile Thr Arg
20 25 30

Ile Arg Gly Thr Ser Tyr Gln Ser Pro His Gly Ile Pro Ile Asp Leu
35 40 45

Leu Asp Arg Leu Leu Ile Val Ser Thr Thr Pro Tyr Ser Glu Lys Asp
50 55 60

Thr Lys Gln Ile Leu Arg Ile Arg Cys Glu Glu Asp Val Glu Met
65 70 75 80

Ser Glu Asp Ala Tyr Thr Val Leu Thr Arg Ile Gly Leu Glu Thr Ser
85 90 95

Leu Arg Tyr Ala Ile Gln Leu Ile Thr Ala Ala Ser Leu Val Cys Arg
100 105 110

Lys Arg Lys Gly Thr Glu Val Gln Val Asp Asp Ile Lys Arg Val Tyr
115 120 125

Ser Leu Phe Leu Asp Glu Ser Arg Ser Thr Gln Tyr Met Lys Glu Tyr
130 135 140

Gln Asp Ala Phe Leu Phe Asn Glu Leu Lys Gly Glu Thr Met Asp Thr
145 150 155 160

Ser

<210> 57
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (42)
<223> Xaa equals stop translation

<400> 57
Met Ala Ser Gly Pro Gly Glu Val Cys Tyr Ser Val Leu Thr Ala Glu
1 5 10 15

His Pro Ala Cys Ile Arg Lys Leu Arg Ser Ser Leu Pro Cys Gln Ile
20 25 30

Asn Leu Asn Gly Pro Cys Pro His Asn Xaa
35 40

<210> 58
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (76)
<223> Xaa equals stop translation

<400> 58
Met Val Leu Pro Ala Thr Gly Gly Leu Arg Val Val Ser Ala Pro Cys
1 5 10 15

Ile Ser Pro Ser Leu Leu Thr Phe Leu Leu Cys Phe Pro Pro Ser Val
20 25 30

Cys Gln Arg Gly Gly Thr Gly Asn Arg Thr Ala Val Ala Ala Leu Ser
35 40 45

Leu Leu Ser Thr Val Tyr Ser Gly Leu Ser Gly Asp Ser Arg Glu Pro
50 55 60

Gly His Leu Ala Ala Val Arg Pro Leu Asn Leu Xaa
65 70 75

<210> 59
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (40)
<223> Xaa equals stop translation

<400> 59
Met Gly Phe Leu Leu Leu Phe Phe Val Ile Ser Ser Thr Cys Tyr Thr
1 5 10 15

Leu Leu Ala Gln Ser Ile Phe Leu Glu His Phe Cys Ile Ser Tyr Gly
20 25 30

Asn Lys Phe Tyr Thr Leu Asp Xaa
35 40

<210> 60
<211> 33

<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (33)
<223> Xaa equals stop translation

<400> 60
Met Leu Ile Asn Val Tyr Leu Phe Ile Ile Phe Val Phe Ile Gln Leu
1 5 10 15

Leu His Ser Ser Phe Leu Arg Leu Gly His Val Asp Thr Tyr Ser Asn
20 25 30

Xaa

<210> 61
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (111)
<223> Xaa equals stop translation

<400> 61
Met Tyr Pro Leu Tyr Cys Lys Ile Leu Leu Ser Phe Leu Phe Leu Leu
1 5 10 15

Leu Ser Ser Asn His Thr Tyr Val Ala Asn His Ile Tyr Ser Phe Trp
20 25 30

Leu Ile Leu Tyr Met Phe Leu Leu Ala Asn Ile Ser Lys Leu Tyr Ile
35 40 45

Phe Asn Ile Leu Thr Tyr Arg Lys Cys Ser Ile Tyr Thr Pro Leu His
50 55 60

Leu Val Phe Leu Phe Val Tyr Leu Arg Ile Tyr Ser Arg Asn His Ser
65 70 75 80

Thr Leu Val His Arg His Leu Phe Asp Tyr Tyr Gly Gln Phe Leu
85 90 95

Lys Trp Leu His Ser Thr Leu Leu Tyr Gly Trp Ile Leu Leu Xaa
100 105 110

<210> 62
<211> 76
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
<222> (76)
<223> Xaa equals stop translation

<400> 62
Met Ile Gly Asp Ile Leu Leu Phe Gly Thr Leu Leu Met Asn Ala Gly
1 5 10 15

Ala Val Leu Asn Phe Lys Leu Lys Lys Asp Thr Gln Gly Phe Gly
20 25 30

Glu Glu Ser Arg Glu Pro Ser Thr Gly Asp Asn Ile Arg Glu Phe Leu
35 40 45

Leu Ser Leu Arg Tyr Phe Arg Ile Phe Ile Ala Leu Trp Asn Ile Phe
50 55 60

Met Met Phe Cys Met Ile Val Leu Phe Gly Ser Xaa
65 70 75

<210> 63
<211> 145
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (145)
<223> Xaa equals stop translation

<400> 63
Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu Leu
1 5 10 15

Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
20 25 30

Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys Asn Thr Leu
35 40 45

Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala Phe Phe Cys Val
50 55 60

Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu Gly Leu Asn Met Pro
65 70 75 80

Leu Leu Ala Tyr His Ile Trp Arg Tyr Met Ser Arg Pro Val Met Ser
85 90 95

Gly Pro Gly Leu Tyr Asp Pro Thr Thr Ile Met Asn Ala Asp Ile Leu
100 105 110

Ala Tyr Cys Gln Lys Glu Gly Trp Cys Lys Leu Ala Phe Tyr Leu Leu
115 120 125

Ala Phe Phe Tyr Tyr Leu Tyr Gly Met Ile Tyr Val Leu Val Ser Ser
130 135 140

Xaa
145

<210> 64
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (45)
<223> Xaa equals stop translation

<400> 64
Met Leu Gln Pro Gly Thr Phe Asn Ser Ile Phe Ser Leu Phe Phe Leu
1 5 10 15

Phe Val Thr Leu Val Phe His Leu Tyr Gln Leu Phe Leu Tyr Leu Leu
20 25 30

Tyr Leu Gln Phe Tyr Lys Leu Pro Gln Ile Leu Phe Xaa
35 40 45

<210> 65
<211> 47
<212> PRT
<213> Homo sapiens

<400> 65
Met Cys Glu Thr Leu Phe Ser Ser Pro Val Ala Leu Gly Thr Asn Tyr
1 5 10 15

Leu Ala Arg Leu Leu Val Phe Val Leu Phe Gln Ala Ala Leu Ser Ser
20 25 30

Gly Val Thr Arg Cys Gln Ser Ala Glu Val Arg Val Lys Lys Thr
35 40 45

<210> 66
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (51)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (83)
<223> Xaa equals stop translation

<400> 66

Met Leu Ile Ala Leu Phe Cys Ile Leu Phe Gln Ile Leu Phe Ser Ile
1 5 10 15

Pro Thr Arg Ile Phe Tyr Ile Phe Leu Ile Asn Lys Arg Val His Ile
20 25 30

Phe Thr Thr Tyr Leu Met Ser Glu Gln Lys Asn His Asp Trp Val Arg
35 40 45

Arg Thr Xaa Lys Leu His Arg Val Trp Leu Ile Ser Gly Lys Met Leu
50 55 60

Leu Val Ala Asp Ile Lys Ala Leu Ile Arg Trp Leu Trp Gly Pro Asn
65 70 75 80

Pro Glu Xaa

<210> 67

<211> 49

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (49)

<223> Xaa equals stop translation

<400> 67

Met Val Arg Lys Lys Leu Gln Ile Thr Ser Ile Leu Ser Gly Leu Lys
1 5 10 15

Leu Phe Leu Leu Ile Leu Trp Ile Asp Trp Leu Val Phe Ala Asn Leu
20 25 30

Ala Leu Ile Gln Leu His Leu Val Gly Arg Val Gly Thr Gly Leu Glu
35 40 45

Xaa

<210> 68

<211> 95

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (92)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (95)

<223> Xaa equals stop translation

<400> 68

Met	Thr	Leu	Leu	Leu	Val	Phe	Ile	Phe	Leu	Pro	Val	Val	Gly	Phe	His
1															
					5				10						15

Gln	Phe	Tyr	Thr	Leu	Gln	Gln	Asn	Ser	Ala	Ile	His	Ser	Gln	Gly	Leu
				20				25							30

Gln	Ile	Pro	Ser	Ser	Ile	Ser	Ser	Leu	Cys	Phe	Leu	Arg	Ile	Ser	Trp
				35			40								45

Leu	Ser	Ile	Leu	Ser	Ser	Pro	Phe	Cys	Phe	Lys	Leu	Asn	Tyr	Pro	Cys
				50			55								60

Phe	Met	Cys	Thr	Tyr	Leu	Phe	Ile	Met	His	Asn	Ile	Ser	Ile	Ile	Phe
	65				70				75						80

Arg	Glu	Leu	Ala	Trp	Glu	Gly	Lys	Met	Asn	Met	Xaa	Ser	Val	Xaa
				85				90						95

<210> 69

<211> 238

<212> PRT

<213> Homo sapiens

<400> 69

Gly	Arg	Pro	Thr	Arg	Pro	Lys	Thr	Pro	Tyr	Asp	Glu	Ser	Lys	Phe	Tyr
	1				5			10							15

Ile	Gly	Cys	Asp	Leu	Cys	Thr	Asn	Trp	Tyr	His	Gly	Glu	Cys	Val	Gly
		20				25									30

Ile	Thr	Glu	Lys	Glu	Ala	Lys	Lys	Met	Asp	Val	Tyr	Ile	Cys	Asn	Asp
	35				40				45						

Cys	Lys	Arg	Ala	Gln	Glu	Gly	Ser	Ser	Glu	Glu	Leu	Tyr	Cys	Ile	Cys
	50				55				60						

Arg	Thr	Pro	Tyr	Asp	Glu	Ser	Gln	Phe	Tyr	Ile	Gly	Cys	Asp	Arg	Cys
	65				70				75						80

Gln	Asn	Trp	Tyr	His	Gly	Arg	Cys	Val	Gly	Ile	Leu	Gln	Ser	Glu	Ala
		85				90									95

Glu	Leu	Ile	Asp	Glu	Tyr	Val	Cys	Pro	Gln	Cys	Gln	Ser	Thr	Glu	Asp
	100				105										110

Ala	Met	Thr	Val	Leu	Thr	Pro	Leu	Thr	Glu	Lys	Asp	Tyr	Glu	Gly	Leu
	115				120										125

Lys	Arg	Val	Leu	Arg	Ser	Leu	Gln	Ala	His	Lys	Met	Ala	Trp	Pro	Phe
	130				135										140

Leu	Glu	Pro	Val	Asp	Pro	Asn	Asp	Ala	Pro	Asp	Tyr	Tyr	Gly	Val	Ile
	145				150				155						160

Lys	Glu	Pro	Met	Asp	Leu	Ala	Thr	Met	Glu	Glu	Arg	Val	Gln	Arg	Arg
	165				170				170						175

Tyr Tyr Glu Lys Leu Thr Glu Phe Val Ala Asp Met Thr Lys Ile Phe
 180 185 190

Asp Asn Cys Arg Tyr Tyr Asn Pro Ser Asp Ser Pro Phe Tyr Gln Cys
 195 200 205

Ala Glu Val Leu Glu Ser Phe Phe Val Gln Lys Leu Lys Gly Phe Lys
 210 215 220

Ala Ser Arg Ser His Asn Asn Lys Leu Gln Ser Thr Ala Ser
 225 230 235

<210> 70

<211> 242

<212> PRT

<213> Homo sapiens

<400> 70

Thr Lys Phe Val Gln Cys Pro Asp Gly Glu Leu Gln Lys Arg Lys Glu
 1 5 10 15

Val Val His Thr Val Ser Leu His Glu Ile Asp Val Ile Asn Ser Arg
 20 25 30

Thr Gln Gly Phe Leu Ala Leu Phe Ser Gly Asp Thr Gly Glu Ile Lys
 35 40 45

Ser Glu Val Arg Glu Gln Ile Asn Ala Lys Val Ala Glu Trp Arg Glu
 50 55 60

Glu Gly Lys Ala Glu Ile Ile Pro Gly Val Leu Phe Ile Asp Glu Val
 65 70 75 80

His Met Leu Asp Ile Glu Ser Phe Ser Phe Leu Asn Arg Ala Leu Glu
 85 90 95

Ser Asp Met Ala Pro Val Leu Ile Met Ala Thr Asn Arg Gly Ile Thr
 100 105 110

Arg Ile Arg Gly Thr Ser Tyr Gln Ser Pro His Gly Ile Pro Ile Asp
 115 120 125

Leu Leu Asp Arg Leu Leu Ile Val Ser Thr Thr Pro Tyr Ser Glu Lys
 130 135 140

Asp Thr Lys Gln Ile Leu Arg Ile Arg Cys Glu Glu Glu Asp Val Glu
 145 150 155 160

Met Ser Glu Asp Ala Tyr Thr Val Leu Thr Arg Ile Gly Leu Glu Thr
 165 170 175

Ser Leu Arg Tyr Ala Ile Gln Leu Ile Thr Ala Ala Ser Leu Val Cys
 180 185 190

Arg Lys Arg Lys Gly Thr Glu Val Gln Val Asp Asp Ile Lys Arg Val
 195 200 205

Tyr Ser Leu Phe Leu Asp Glu Ser Arg Ser Thr Gln Tyr Met Lys Glu
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Thr Ser Ser Phe Cys Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp
20 25 30

Pro Xaa Pro Glu Cys Arg Gly Lys Ser
35 40

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International application No. PCT/US98/17709

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07H 21/00; C12N 5/10, 15/09, 15/10, 15/12, 15/63

US CL :435/320.1, 325, 252.3, 254.11; 536/23.5

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/320.1, 325, 252.3, 254.11; 536/23.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

GENBANK, EMBL, SWISS-PROT

search: SEQ ID NO: 11-20, 40-49

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database GENBANK, US National Library of Medicine, (Bethesda, MD, USA), No. B01406, EVANS et al., 'Genomic sequence sampled map of chromosome 11', complete record, 26 January 1996, see entire abstract.	1, 7-10
X	Database GENBANK, US National Library of Medicine, (Bethesda, MD, USA), No. H04658, HILLIER et al., 'The WashU-Merck EST Project', complete record, 20 June 1995, see entire abstract.	1, 7-10
X	Database GENBANK, US National Library of Medicine, (Bethesda, MD, USA), No. AA253014, HILLIER et al., 'WashU-Merck EST Project 1997', complete record, 06 August 1997, see entire abstract.	1, 7-10

Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents:	'T'	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	'X'	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	'Y'	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	'&'	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 09 NOVEMBER 1998	Date of mailing of the international search report 29 DEC 1998
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Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer SCOTT D. PRIEBE Telephone No. (703) 308-0196
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INTERNATIONAL SEARCH REPORT

International application No. PCT/US98/17709

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database GENBANK, US National Library of Medicine, (Bethesda, MD, USA), No. AA184809, MARRA et al., 'The WashU-HHMI Mouse EST Project', complete record, 07 January 1997, see entire document.	1, 7-10
X	Database GENBANK, US National Library of Medicine, (Bethesda, MD, USA), No. H97682, HILLIER et al., 'The WashU-Merck EST Project', complete record, 12 December 1995, see entire document.	1, 7-10
X	Database GENBANK, US National Library of Medicine, (Bethesda, MD, USA), No. R77507, HILLIER et al., 'The WashU-Merck EST Project', complete record, 07 June 1995, see entire document.	1, 7-10
X	Database GENBANK, US National Library of Medicine, (Bethesda, MD, USA), No. AA530982, NCI-CGAP, 'National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index', complete record, 20 August 1997, see entire document.	1, 7-10
X	Database GENBANK, US National Library of Medicine, (Bethesda, MD, USA), No. AA312632, ADAMS et al., 'Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence', complete record, 19 April 1997, see entire document.	1, 7-10
X	Database GENBANK, US National Library of Medicine, (Bethesda, MD, USA), No. AA459132, NCI-CGAP, 'National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index', complete record, 13 August 1997, see entire document.	1, 7-10
X	Database GENBANK, US National Library of Medicine, (Bethesda, MD, USA), No. R05785, HILLIER et al., 'The WashU-Merck EST Project', complete record, 03 April 1995, see entire document.	1, 7-10
X	DWYER et al. Structure and expression of AtS1, an <i>Arabidopsis thaliana</i> gene homologous to the S-locus related genes of <i>Brassica</i> . Molecular and General Genetics. 1992, Vol. 231, pages 442-448, especially pages 442, 443 and 445.	1, 2, 7-10
X	LAUDER et al. Dual requirement for the yeast MMS19 gene in DNA repair and RNA polymerase II transcription. Molecular and Cellular Biology. December 1996, Vol. 16, No. 12, pages 6783-6786.	1, 7-10

INTERNATIONAL SEARCH REPORT

<p>International application No. PCT/US98/17709</p>

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ZOCK et al. The <i>Bacillus subtilis</i> pnbA gene encoding p-nitrobenzyl esterase: cloning, sequence and high level expression in <i>Escherichia coli</i> . <i>Gene</i> . 1994, Vol. 151, pages 37-43, especially pages 40-41.	1, 7-10
X	COLAS et al. <i>Drosophila</i> 5-HT2 serotonin receptor: coexpression with fushi-tarazu during segmentation. <i>Proceedings of the National Academy of Science USA</i> . June 1995, Vol. 92, pages 5441-5445, especially pages 5441-5442.	1, 2, 7-10
X	LIN et al. Isolation and characterization of C-reactive protein (CRP) cDNA and genomic DNA from <i>Xenopus laevis</i> . <i>Journal of Biological Chemistry</i> . 25 March 1993, Vol. 268, No. 9, pages 6809-6815, especially pages 6809, 6810-6811 and 6813.	1, 2, 7-10
X	TANAKA et al. Molecular cloning of cDNA for vacuolar membrane proton-translocating inorganic pyrophosphatase in <i>Hordeum vulgare</i> . <i>Biochemical and Biophysical Research Communications</i> . 15 February 1993, Vol. 190, No. 3, pages 1110-1114, especially pages 1110-1112.	1, 2, 7-10
X	EVERS et al. Molecular coevolution of mammalian ribosomal gene terminator sequences and the transcription termination factor TTF-1. <i>Proceedings of the National Academy of Science USA</i> . June 1995, Vol. 92, pages 5827-5831, especially pages 5827-5828.	1, 7-10
X	PASQUALONE et al. STU1, a suppressor of a beta-tubulin mutation, encodes a novel and essential component of the yeast mitotic spindle. <i>Journal of Cell Biology</i> . December 1994, Vol. 127, No. 6, Part 2, pages 1973-1985, especially pages 1974-1975 and 1980.	1, 7-10

INTERNATIONAL SEARCH REPORTInternational application No.
PCT/US98/17709**BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING**

This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Group I, claim(s) 1-10, 21, drawn to polynucleotides comprising or hybridizing to a polynucleotide comprising SEQ ID NO: X or encoding SEQ ID NO: Y; vectors and cells comprising the same. Additionally, Group I contains the first claimed method of using the polynucleotide (claim 8) to make a cell. There are a total of 29 polynucleotides, SEQ ID NO: X, and corresponding polypeptides, SEQ ID NO: Y of which the first ten (10) are selected for examination (SEQ ID NO: 11-20) as Group I. There are an additional nineteen (19) polynucleotides, and therefore five (5) remaining additional groups of not more than four (4) polynucleotide sequences each.

Group II, claim(s) 11, 12, 14-16, drawn to polypeptides of SEQ ID NO: Y or encoded by the heterologous DNA of ATCC Deposit No. Z. Additionally, Group II includes a recombinant host cell expressing the polypeptide (claim 14) and a method of making the polypeptide using same (claim 15). It is noted that claim 14 does not require that the polypeptide be expressed from any heterologous DNA present in the cell, therefore the pre-existing cell genome could comprise its own gene therefore for expressing the polypeptide. The first polypeptide, SEQ ID NO: Y is selected for examination with group II; there are an additional 28 remaining polypeptides, and therefore an additional 28 groups within group II.

Group III, claim(s) 13, drawn to an antibody to a polypeptide of SEQ ID NO: Y. An antibody to the first polypeptide, SEQ ID NO: Y is selected for examination with group II; there are an additional 28 remaining antibodies, and therefore an additional 28 groups within group III.

Group IV, claim(s) 17, drawn to a method of treatment with a polypeptide, SEQ ID NO: Y, of Group II. The first polypeptide, SEQ ID NO: Y is selected for examination with group II; there are an additional 28 remaining polypeptides, and therefore an additional 28 groups within group IV.

Group V, claim(s) 17, drawn to a method of treatment with a polynucleotide of Group I. There are a total of 29 polynucleotides, SEQ ID NO: X, and corresponding polypeptides, SEQ ID NO: Y of which the first ten (10) are selected for examination. There are an additional nineteen (19) polynucleotides, and therefore five (5) remaining additional groups of not more than four (4) polynucleotide sequences each within group V.

Group VI, claim(s) 18, drawn to a diagnostic method comprising identifying a mutation in a polynucleotide of group I. There are a total of 29 polynucleotides, SEQ ID NO: X, and corresponding polypeptides, SEQ ID NO: Y of which the first ten (10) are selected for examination. There are an additional nineteen (19) polynucleotides, and therefore five (5) remaining additional groups of not more than four (4) polynucleotide sequences each within group VI.

Group VII, claim(s) 19, drawn to a diagnostic method comprising measuring amount of a polypeptide of group II. The first polypeptide, SEQ ID NO: Y is selected for examination with group II; there are an additional 28 remaining polypeptides, and therefore an additional 28 groups within group VII.

Group VIII, claim(s) 20, drawn to a method for identifying a ligand that binds a polypeptide of group II. The first polypeptide, SEQ ID NO: Y is selected for examination with group II; there are an additional 28 remaining polypeptides, and therefore an additional 28 groups within group VIII.

Group IX, claim(s) 22, drawn to a method of identifying the biological activity of a polypeptide of SEQ ID NO: Y. The first polypeptide, SEQ ID NO: Y is selected for examination with group II; there are an additional 28 remaining polypeptides, and therefore an additional 28 groups within group IX.

The inventions listed as Groups I through IX do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons.

Claims of groups I, V, and VI are drawn to polynucleotides, polynucleotide constructs or methods requiring the use of same that contain more than ten (10) individual, independent and distinct nucleotide sequences in alternative form. Accordingly, these claims are subject to lack of unity as outlined in 1192 O.G. 68 (19 November 1996). The first ten (10) individual polynucleotide sequences designated "X" in the table on pages 45-48 of the description selected by applicant are included for search. The corresponding SEQ ID NO: Y and ATCC deposit number "Z" for each selected

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"X" are likewise selected for search. The search of no more than ten (10) sequences may include the complements of the selected sequences and, where appropriate, may include subsequences within the selected sequences, e.g. probes and primers. Applicant has selected the first ten (10) polynucleotide sequences, i.e. SEQ ID NOs 11-20 from the table.

As to the polypeptides of group II or the antibodies thereto of group III, or the alternative methods of using the polypeptides of groups IV, VII, VIII and IX, each individual polypeptide is a different and distinct invention.

Each of the polynucleotides, SEQ ID NO: X, encodes a polypeptide, SEQ ID NO: Y, that, absent evidence to the contrary, is structurally and functionally distinct with different chemical, physical and biological properties. For example see the descriptions of the 29 different genes on pages 5-44 of the description. Each are directed to genes encoding different proteins, expressed in different cells, mapping to different chromosomes, and are therefore distinct and different polynucleotides not sharing any special technical feature. Likewise, the polypeptides SEQ ID NO: Y and antibodies of group III are distinct and different proteins, not sharing any special technical features.

Each of the groups IV to IX are directed to alternative uses of some, but not all, of the products of groups I or II. In so much as each group encompasses a multitude of different inventions *vis a vis* the different polynucleotides or polypeptides, each group fails to share the same special technical features throughout the scope of each group.

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